

SEQUENCE LISTING

(1) GENERAL INFORMATION

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- 10 (ii) TITLE OF THE INVENTION: RANDOM PEPTIDES THAT BIND TO GASTRO-  
INTESTINAL TRACT (GIT) TRANSPORT RECEPTORS AND RELATED METHODS
- (iii) NUMBER OF SEQUENCES: 407
- (iv) CORRESPONDENCE ADDRESS:  
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15 (E) COUNTRY: USA  
(F) ZIP: 10036
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ Version 2.0
- 20 (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 09/079,819  
(B) FILING DATE: May 15, 1998  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:  
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- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 44 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
30 (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Arg Ser Gly Ala Tyr Glu Ser Pro Asp Gly Arg Gly Gly Arg Ser Tyr  
1 5 10 15  
Val Gly Gly Gly Gly Gly Cys Gly Asn Ile Gly Arg Lys His Asn Leu  
20 25 30  
Trp Gly Leu Arg Thr Ala Ser Pro Ala Cys Trp Asp  
35 40

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ser Pro Arg Ser Phe Trp Pro Val Val Ser Arg His Glu Ser Phe Gly  
1 5 10 15  
Ile Ser Asn Tyr Leu Gly Cys Gly Tyr Arg Thr Cys Ile Ser Gly Thr  
20 25 30  
Met Thr Lys Ser Ser Pro Ile Tyr Pro Arg His Ser  
35 40

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ser Ser Ser Ser Asp Trp Gly Gly Val Pro Gly Lys Val Val Arg Glu  
1 5 10 15  
Arg Phe Lys Gly Arg Gly Cys Gly Ile Ser Ile Thr Ser Val Leu Thr  
20 25 30  
Gly Lys Pro Asn Pro Cys Pro Glu Pro Lys Ala Ala  
35 40

(2) INFORMATION FOR SEQ ID NO:4:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

30

Arg Val Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala Arg  
1 5 10 15

Ser Cys Ala His Gln Gly Cys Gly Ala Gly Thr Arg Asn Ser His Gly  
 20 25 30  
 Cys Ile Thr Arg Pro Leu Arg Gln Ala Ser Ala His  
 35 40

(2) INFORMATION FOR SEQ ID NO:5:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

10 Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe Arg Glu  
 1 5 10 15  
 Leu Arg Asp Arg Trp Asn Ala Thr Ser His His Thr Arg Pro Thr Pro  
 20 25 30  
 Gln Leu Pro Arg Gly Pro Asn  
 35

(2) INFORMATION FOR SEQ ID NO:6:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 41 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

20 Ser Pro Cys Gly Gly Ser Trp Gly Arg Phe Met Gln Gly Gly Leu Phe  
 1 5 10 15  
 Gly Gly Arg Thr Asp Gly Cys Gly Ala His Arg Asn Arg Thr Ser Ala  
 20 25 30  
 Ser Leu Glu Pro Pro Ser Ser Asp Tyr  
 35 40

(2) INFORMATION FOR SEQ ID NO:7:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

30 Arg Gly Ala Ala Asp Gln Arg Arg Gly Trp Ser Glu Asn Leu Gly Leu  
 1 5 10 15  
 Pro Arg Val Gly Trp Asp Ala Ile Ala His Asn Ser Tyr Thr Phe Thr  
 20 25 30  
 Ser Arg Arg Pro Arg Pro Pro  
 35

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Gly Gly Glu Val Ser Ser Trp Gly Arg Val Asn Asp Leu Cys Ala  
1 5 10 15  
Arg Val Ser Trp Thr Gly Cys Gly Thr Ala Arg Ser Ala Arg Thr Asp  
20 25 30  
Asn Lys Gly Phe Leu Pro Lys His Ser Ser Leu Arg  
35 40

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(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ser Asp Ser Asp Gly Asp His Tyr Gly Leu Arg Gly Gly Val Arg Cys  
1 5 10 15  
Ser Leu Arg Asp Arg Gly Cys Gly Leu Ala Leu Ser Thr Val His Ala  
20 25 30  
Gly Pro Pro Ser Phe Tyr Pro Lys Leu Ser Ser Pro  
35 40

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(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Arg Ser Leu Gly Asn Tyr Gly Val Thr Gly Thr Val Asp Val Thr Val  
1 5 10 15  
Leu Pro Met Pro Gly His Ala Asn His Leu Gly Val Ser Ser Ala Ser  
20 25 30  
Ser Ser Asp Pro Pro Arg Arg  
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(2) INFORMATION FOR SEQ ID NO:11:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids

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(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

5 Arg Thr Thr Thr Ala Lys Gly Cys Leu Leu Gly Ser Phe Gly Val Leu  
1 5 10 15  
Ser Gly Cys Ser Phe Thr Pro Thr Ser Pro Pro Pro His Leu Gly Tyr  
20 25 30  
Pro Pro His Ser Val Asn  
35

(2) INFORMATION FOR SEQ ID NO:12:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

15 Ser Pro Lys Leu Ser Ser Val Gly Val Met Thr Lys Val Thr Glu Leu  
1 5 10 15  
Pro Thr Glu Gly Pro Asn Ala Ile Ser Ile Pro Ile Ser Ala Thr Leu  
20 25 30  
Gly Pro Arg Asn Pro Leu Arg  
35

(2) INFORMATION FOR SEQ ID NO:13:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

25 Arg Trp Cys Gly Ala Glu Leu Cys Asn Ser Val Thr Lys Lys Phe Arg  
1 5 10 15  
Pro Gly Trp Arg Asp His Ala Asn Pro Ser Thr His His Arg Thr Pro  
20 25 30  
Pro Pro Ser Gln Ser Ser Pro  
35

(2) INFORMATION FOR SEQ ID NO:14:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 44 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Arg Trp Cys Gly Ala Asp Asp Pro Cys Gly Ala Ser Arg Trp Arg Gly  
1 5 10 15  
Gly Asn Ser Leu Phe Gly Cys Gly Leu Arg Cys Ser Ala Ala Gln Ser  
20 25 30  
5 Thr Pro Ser Gly Arg Ile His Ser Thr Ser Thr Ser  
35 40

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ser Lys Ser Gly Glu Gly Gly Asp Ser Ser Arg Gly Glu Thr Gly Trp  
1 5 10 15  
Ala Arg Val Arg Ser His Ala Met Thr Ala Gly Arg Phe Arg Trp Tyr  
20 25 30  
15 Asn Gln Leu Pro Ser Asp Arg  
35

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Arg Ser Ser Ala Asn Asn Cys Glu Trp Lys Ser Asp Trp Met Arg Arg  
1 5 10 15  
Ala Cys Ile Ala Arg Tyr Ala Asn Ser Ser Gly Pro Ala Arg Ala Val  
20 25 30  
Asp Thr Lys Ala Ala Pro  
35

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(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NC:17:

Ser Lys Trp Ser Trp Ser Ser Arg Trp Gly Ser Pro Gln Asp Lys Val  
 1 5 10 15  
 Glu Lys Thr Arg Ala Gly Cys Gly Gly Ser Pro Ser Ser Thr Asn Cys  
 20 25 30  
 His Pro Tyr Thr Phe Ala Pro Pro Pro Gln Ala Gly  
 35 40

(2) INFORMATION FOR SEQ ID NO:18:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

10

Ser Gly Phe Trp Glu Phe Ser Arg Gly Leu Trp Asp Gly Glu Asn Arg  
 1 5 10 15  
 Lys Ser Val Arg Ser Gly Cys Gly Phe Arg Gly Ser Ser Ala Gln Gly  
 20 25 30  
 Pro Cys Pro Val Thr Pro Ala Thr Ile Asp Lys His  
 35 40

(2) INFORMATION FOR SEQ ID NO:19:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

20

Ser Glu Ser Gly Arg Cys Arg Ser Val Ser Arg Trp Met Thr Thr Trp  
 1 5 10 15  
 Gln Thr Gln Lys Gly Gly Cys Gly Ser Asn Val Ser Arg Gly Ser Pro  
 20 25 30  
 Leu Asp Pro Ser His Gln Thr Gly His Ala Thr Thr  
 35 40

(2) INFORMATION FOR SEQ ID NO:20:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Arg Glu Trp Arg Phe Ala Gly Pro Pro Leu Asp Leu Trp Ala Gly Pro  
 1 5 10 15  
 Ser Leu Pro Ser Phe Asn Ala Ser Ser His Pro Arg Ala Leu Arg Thr  
 20 25 30

Tyr Trp Ser Gln Arg Pro Arg  
35

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Arg Met Glu Asp Ile Lys Asn Ser Gly Trp Arg Asp Ser Cys Arg Trp  
1 5 10 15  
Gly Asp Leu Arg Pro Gly Cys Gly Ser Arg Gln Trp Tyr Pro Ser Asn  
20 25 30  
Met Arg Ser Ser Arg Asp Tyr Pro Ala Gly Gly His  
35 40

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ser His Pro Trp Tyr Arg His Trp Asn His Gly Asp Phe Ser Gly Ser  
1 5 10 15  
Gly Gln Ser Arg His Thr Pro Pro Glu Ser Pro His Pro Gly Arg Pro  
20 25 30  
Asn Ala Thr Ile  
35

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Arg Tyr Lys His Asp Ile Gly Cys Asp Ala Gly Val Asp Lys Lys Ser  
1 5 10 15  
Ser Ser Val Arg Gly Gly Cys Gly Ala His Ser Ser Pro Pro Arg Ala  
20 25 30  
Gly Arg Gly Pro Arg Gly Thr Met Val Ser Arg Leu  
35 40

(2) INFORMATION FOR SEQ ID NO:24:



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ser	Gln	Gly	Ser	Lys	Gln	Cys	Met	Gln	Tyr	Arg	Thr	Gly	Arg	Leu	Thr
1				5					10					15	
Val	Gly	Ser	Glu	Tyr	Gly	Cys	Gly	Met	Asn	Pro	Ala	Arg	His	Ala	Thr
			20					25					30		
Pro	Ala	Tyr	Pro	Ala	Arg	Leu	Leu	Pro	Arg	Tyr	Arg				
		35					40								

(2) INFORMATION FOR SEQ ID NO:25:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

15

Ser	Gly	Arg	Thr	Thr	Ser	Glu	Ile	Ser	Gly	Leu	Trp	Gly	Trp	Gly	Asp
1				5					10					15	
Asp	Arg	Ser	Gly	Tyr	Gly	Trp	Gly	Asn	Thr	Leu	Arg	Pro	Asn	Tyr	Ile
			20					25					30		
Pro	Tyr	Arg	Gln	Ala	Thr	Asn	Arg	His	Arg	Tyr	Thr				
		35					40								

(2) INFORMATION FOR SEQ ID NO:26:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

25

Arg	Trp	Asn	Trp	Thr	Val	Leu	Pro	Ala	Thr	Gly	Gly	His	Tyr	Trp	Thr
1				5					10					15	
Arg	Ser	Thr	Asp	Tyr	His	Ala	Ile	Asn	Asn	His	Arg	Pro	Ser	Ile	Pro
			20					25					30		
His	Gln	His	Pro	Thr	Pro	Ile									
		35													

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

30

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

5 Ser Trp Ser Ser Trp Asn Trp Ser Ser Lys Thr Thr Arg Leu Gly Asp  
1 5 10 15  
Arg Ala Thr Arg Glu Gly Cys Gly Pro Ser Gln Ser Asp Gly Cys Pro  
20 25 30  
Tyr Asn Gly Arg Leu Thr Thr Val Lys Pro Arg Thr  
35 40

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 37 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

15 Ser Gly Ser Leu Asn Ala Trp Gln Pro Arg Ser Trp Val Gly Gly Ala  
1 5 10 15  
Phe Arg Ser His Ala Asn Asn Asn Leu Asn Pro Lys Pro Thr Met Val  
20 25 30  
Thr Arg His Pro Thr  
35

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 44 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

25 Arg Tyr Ser Gly Leu Ser Pro Arg Asp Asn Gly Pro Ala Cys Ser Gln  
1 5 10 15  
Glu Ala Thr Leu Glu Gly Cys Gly Ala Gln Arg Leu Met Ser Thr Arg  
20 25 30  
Arg Lys Gly Arg Asn Ser Arg Pro Gly Trp Thr Leu  
35 40

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 39 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ser Val Gly Asn Asp Lys Thr Ser Arg Pro Val Ser Phe Tyr Gly Arg  
1 5 10 15  
Val Ser Asp Leu Trp Asn Ala Ser Leu Met Pro Lys Arg Thr Pro Ser  
20 25 30  
Ser Lys Arg His Asp Asp Gly  
35

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(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Arg Trp Pro Ser Val Gly Tyr Lys Gly Asn Gly Ser Asp Thr Ile Asp  
1 5 10 15  
Val His Ser Asn Asp Ala Ser Thr Lys Arg Ser Leu Ile Tyr Asn His  
20 25 30  
Arg Arg Pro Leu Phe Pro  
35

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(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Arg Thr Phe Glu Asn Asp Gly Leu Gly Val Gly Arg Ser Ile Gln Lys  
1 5 10 15  
Lys Ser Asp Arg Trp Tyr Ala Ser His Asn Ile Arg Ser His Phe Ala  
20 25 30  
Ser Met Ser Pro Ala Gly Lys  
35

(2) INFORMATION FOR SEQ ID NO:33:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

30

Ser Tyr Cys Arg Val Lys Gly Gly Gly Glu Gly Gly His Thr Asp Ser  
1 5 10 15

Asn Leu Ala Arg Ser Gly Cys Gly Lys Val Ala Arg Thr Ser Arg Leu  
 20 25 30  
 Gln His Ile Asn Pro Arg Ala Thr Pro Pro Ser Arg  
 35 40

(2) INFORMATION FOR SEQ ID NO:34:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

10 Ser Trp Thr Arg Trp Gly Lys His Thr His Gly Gly Phe Val Asn Lys  
 1 5 10 15  
 Ser Pro Pro Gly Lys Asn Ala Thr Ser Pro Tyr Thr Asp Ala Gln Leu  
 20 25 30  
 Pro Ser Asp Gln Gly Pro Pro  
 35

(2) INFORMATION FOR SEQ ID NO:35:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 44 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

20 Ser Gln Val Asp Ser Phe Arg Asn Ser Phe Arg Trp Tyr Glu Pro Ser  
 1 5 10 15  
 Arg Ala Leu Cys His Gly Cys Gly Lys Arg Asp Thr Ser Thr Arg  
 20 25 30  
 Ile His Asn Ser Pro Ser Asp Ser Tyr Pro Thr Arg  
 35 40

(2) INFORMATION FOR SEQ ID NO:36:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

30 Ser Phe Leu Arg Phe Gln Ser Pro Arg Phe Glu Asp Tyr Ser Arg Thr  
 1 5 10 15  
 Ile Ser Arg Leu Arg Asn Ala Thr Asn Pro Ser Asn Val Ser Asp Ala  
 20 25 30  
 His Asn Asn Arg Ala Leu Ala  
 35

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Arg Ser Ile Thr Asp Gly Gly Ile Asn Glu Val Asp Leu Ser Ser Val  
1 5 10 15  
Ser Asn Val Leu Glu Asn Ala Asn Ser His Arg Ala Tyr Arg Lys His  
20 25 30  
Arg Pro Thr Leu Lys Arg Pro  
35

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(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ser Ser Lys Val Ser Ser Pro Arg Asp Pro Thr Val Pro Arg Lys Gly  
1 5 10 15  
Gly Asn Val Asp Tyr Gly Cys Gly His Arg Ser Ser Ala Arg Met Pro  
20 25 30  
Thr Ser Ala Leu Ser Ser Ile Thr Lys Cys Tyr Thr  
35 40

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(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

25

Arg Ala Ser Thr Gln Gly Gly Arg Gly Val Ala Pro Glu Phe Gly Ala  
1 5 10 15  
Ser Val Leu Gly Arg Gly Cys Gly Ser Ala Thr Tyr Tyr Thr Asn Ser  
20 25 30  
Thr Ser Cys Lys Asp Ala Met Gly His Asn Tyr Ser  
35 40

(2) INFORMATION FOR SEQ ID NO:40:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids

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(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

5 Arg Trp Cys Glu Lys His Lys Phe Thr Ala Ala Arg Cys Ser Ala Gly  
1 5 10 15  
Ala Gly Phe Glu Arg Asp Ala Ser Arg Pro Pro Gln Pro Ala His Arg  
20 25 30  
Asp Asn Thr Asn Arg Asn Ala  
35

(2) INFORMATION FOR SEQ ID NO:41:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

15 Ser Phe Gln Val Tyr Pro Asp His Gly Leu Glu Arg His Ala Leu Asp  
1 5 10 15  
Gly Thr Gly Pro Leu Tyr Ala Met Pro Gly Arg Trp Ile Arg Ala Arg  
20 25 30  
Pro Gln Asn Arg Asp Arg Gln  
35

(2) INFORMATION FOR SEQ ID NO:42:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

25 Ser Arg Cys Thr Asp Asn Glu Gln Cys Pro Asp Thr Gly Thr Arg Ser  
1 5 10 15  
Arg Ser Val Ser Asn Ala Arg Tyr Phe Ser Ser Arg Leu Leu Lys Thr  
20 25 30  
His Ala Pro His Arg Pro  
35

(2) INFORMATION FOR SEQ ID NO:43:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Ser Ala Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val Arg  
1 5 10 15  
Leu Asn Gly Val Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn  
20 25 30  
5 Pro Arg Gly Arg Arg His Pro  
35

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Ser Ser Ala Asp Ala Glu Lys Cys Ala Gly Ser Leu Leu Trp Trp Gly  
1 5 10 15  
Arg Gln Asn Asn Ser Gly Cys Gly Ser Pro Thr Lys Lys His Leu Lys  
20 25 30  
15 His Arg Asn Arg Ser Gln Thr Ser Ser Ser Ser His  
35 40

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

20

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Arg Pro Lys Asn Val Ala Asp Ala Tyr Ser Ser Gln Asp Gly Ala Ala  
1 5 10 15  
Ala Glu Glu Thr Ser His Ala Ser Asn Ala Ala Arg Lys Ser Pro Lys  
20 25 30  
His Lys Pro Leu Arg Arg Pro  
35

25

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Arg Gly Ser Thr Gly Thr Ala Gly Gly Glu Arg Ser Gly Val Leu Asn  
 1 5 10 15  
 Leu His Thr Arg Asp Asn Ala Ser Gly Ser Gly Phe Lys Pro Trp Tyr  
 20 25 30  
 Pro Ser Asn Arg Gly His Lys  
 35

(2) INFORMATION FOR SEQ ID NO:47:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

10

Arg Trp Gly Trp Glu Arg Ser Pro Ser Asp Tyr Asp Ser Asp Met Asp  
 1 5 10 15  
 Leu Gly Ala Arg Arg Tyr Ala Thr Arg Thr His Arg Ala Pro Pro Arg  
 20 25 30  
 Val Leu Lys Ala Pro Leu Pro  
 35

(2) INFORMATION FOR SEQ ID NO:48:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

20

Arg Gly Trp Lys Cys Glu Gly Ser Gln Ala Ala Tyr Gly Asp Lys Asp  
 1 5 10 15  
 Ile Gly Arg Ser Arg Gly Cys Gly Ser Ile Thr Lys Asn Asn Thr Asn  
 20 25 30  
 His Ala His Pro Ser His Gly Ala Val Ala Lys Ile  
 35 40

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

30

Ser Arg Glu Glu Ala Asn Trp Asp Gly Tyr Lys Arg Glu Met Ser His  
 1 5 10 15  
 Arg Ser Arg Phe Trp Asp Ala Thr His Leu Ser Arg Pro Arg Arg Pro  
 20 25 30



Ala Asn Ser Gly Asp Pro Asn  
35

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

10 Glu Trp Tyr Ser Trp Lys Arg Ser Ser Lys Ser Thr Gly Leu Gly Asp  
1 5 10 15  
Thr Ala Thr Arg Glu Gly Cys Gly Pro Ser Gln Ser Asp Gly Cys Pro  
20 25 30  
Tyr Asn Gly Arg Leu Thr Thr Val Lys Pro Arg Lys  
35 40

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

20 Arg Glu Phe Ala Glu Arg Arg Leu Trp Gly Cys Asp Asp Leu Ser Trp  
1 5 10 15  
Arg Leu Asp Ala Glu Gly Cys Gly Pro Thr Pro Ser Asn Arg Ala Val  
20 25 30  
Lys His Arg Lys Pro Arg Pro Arg Ser Pro Ala Leu  
35 40

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

30 Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys Glu  
1 5 10 15  
Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg Lys  
20 25 30  
Val Phe Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr  
35 40

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Arg	His	Ile	Ser	Glu	Tyr	Ser	Phe	Ala	Asn	Ser	His	Leu	Met	Gly	Gly
1				5					10					15	
Glu	Ser	Lys	Arg	Lys	Gly	Cys	Gly	Ile	Asn	Gly	Ser	Phe	Ser	Pro	Thr
		20					25						30		
Cys	Pro	Arg	Ser	Pro	Thr	Pro	Ala	Phe	Arg	Arg	Thr				
		35					40								

(2) INFORMATION FOR SEQ ID NO:54:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

15

Ser	Arg	Glu	Ser	Gly	Met	Trp	Gly	Ser	Trp	Trp	Arg	Gly	His	Arg	Leu
1				5				10					15		
Asn	Ser	Thr	Gly	Gly	Asn	Ala	Asn	Met	Asn	Ala	Ser	Leu	Pro	Pro	Asp
		20					25					30			
Pro	Pro	Val	Ser	Thr	Pro										
		35													

(2) INFORMATION FOR SEQ ID NO:55:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

25

Ser	Thr	Pro	Pro	Ser	Arg	Glu	Ala	Tyr	Ser	Arg	Pro	Tyr	Ser	Val	Asp
1				5				10					15		
Ser	Asp	Ser	Asp	Thr	Asn	Ala	Lys	His	Ser	Ser	His	Asn	Arg	Arg	Leu
		20					25					30			
Arg	Thr	Arg	Ser	Arg	Pro	Asn									
		35													

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

30

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

	TCTCACTCCT	CGAGATCCGG	CGCTTATGAG	AGTCCGGATG	GTCGGGGGGG	TCGGAGCTAT	60
	GTGGGGGGCG	GGGGTGGNTG	TGGTAACATT	GGTCGGAAGC	ATAACCTGTG	GGGGCTGCGT	120
5	ACCGCGTCGC	CGGCCTGCTG	GGACTCTAGA	ATCGAAGGTC	GCGCTAGACC	TTCGAGA	177

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

	TCTCACTCCT	CGAGTCCTCG	CTCTTTCTGG	CCC GTTGTGT	CCCGGCATGA	GTCGTTTGGG	60
	ATCTCTAACT	ATTTGGGNTG	TGGTTATCGT	ACATGTATCT	CCGGCACGAT	GACTAAGTCT	120
	AGCCCCGATTT	ACCCTCGGCA	TTCGTCTAGA	ATCGAAGGTC	GCGCTAGACC	TTCGAGA	177

(2) INFORMATION FOR SEQ ID NO:58:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

	TCTCACTCCT	CGAGTAGTAG	CTCCGATTGG	GGTGGTGTGC	CTGGGAAGGT	GGTTAGGGAG	60
	CGCTTTAAGG	GGCGCGGTTG	TGGTATTTCC	ATCACCTCCG	TGCTCACTGG	GAAGCCCAAT	120
20	CCGTGTCCGG	AGCCTAAGGC	GGCCTCTAGA	ATCGAAGGTC	GCGCTAGACC	TTCGAGA	177

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

	TCTCACTCCT	CGAGAGTTGG	CCAGTGCACG	GATTCTGATG	TGCGGCGTCC	TTGGGCCAGG	60
	TCTTGCGCTC	ATCAGGGTTG	TGGTGCGGGC	ACTCGCAACT	CGCACGGCTG	CATCACCCGT	120
	CCTCTCCGCC	AGGCTAGCGC	TCATTCTAGA	ATCGAAGGTC	GCGCTAGACC	TTCGAGA	177

(2) INFORMATION FOR SEQ ID NO:60:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

5

TCTCACTCCT CGAGCCACTC CGGTGGTATG AATAGGGCCT ACGGGGATGT GTTTAGGGAG 60  
CTTCGTGATC GGTGGAACGC CACTTCCCAC CACACTCGCC CCACCCCTCA GCTCCCCCGT 120  
GGGCCTAATT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TCTCACTCCT CGAGTCCGTG CGGGGGGTCG TGGGGGCGTT TTATGCAGGG TGGCCTTTTC 60  
GGCGGTAGGA CTGATGGTTG TGGTGCCCAT AGAAACCGCA CTTCGCGTC GTTAGAGCCC 120  
CCGAGCAGCG ACTACTCTAG AATCGAAGGT CGCGCTAGAC CTTCGAGA 168

15

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TCTCACTCCT CGAGGGGCGC CGCCGATCAG CGGCGGGGGT GGTCCGAGAA CTTGGGGTTG 60  
CCTAGGGTGG GGTGGGACGC CATCGCTCAC AATAGCTATA CGTTCACCTC GCGCCGCCCCG 120  
CGCCCCCCT CTAGA 135

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

30 TCTCACTCCT CGAGCGGTGG GGAGGTCAGC TCCTGGGGCC GCGTGAATGA CCTCTGCGCT 60  
AGGGTGAGTT GGACTGGTTG TGGTACTGCT CGTTCCGCGC GTACCGACAA CAAAGGCTTT 120  
CTTCCTAAGC ACTCGTCACT CCGCTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA 177

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

TCTCACTCCT	CGAGTGATAG	TGACGGGGAT	CATTATGGGC	TTCGGGGGGG	GGTGCGTTGT	60
TCGCTTCGTG	ATAGGGGTTG	TGGTCTGGCC	CTGTCCACCG	TCCATGCTGG	TCCCCCTCT	120
TTTACCCCA	AGCTCTCCAG	CCCCTCTAGA	ATCGAAGGTC	GCGCTAGACC	TTCGAGA	177

(2) INFORMATION FOR SEQ ID NO:65:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TCTCACTCCT	CGAGGAGCTT	GGGTAATTAT	GGCGTCACCG	GGACTGTGGA	CGTGACGGTT	60
TTGCCCATGC	CTGGCCACGC	CAACCACCTT	GGTGTCTCCT	CCGCCTCTAG	CTCTGATCCT	120
CCGCGGCGCT	CTAGAATCGA	AGGTCGCGCT	AGACCTTCGA	GA		162

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

TCTCACTCCT	CGAGAACTAC	GACGGCTAAG	GGGTGTCTTC	TCGGAAGCTT	CGGCGTTCTT	60
AGTGGGTGCT	CATTTACGCC	AACCTCTCCA	CCGCCCCACC	TAGGATACCC	CCCCCACTCC	120
GTCAATTCTA	GAATCGAAGG	TCGCGCTAGA	CCTTCGAGA			159

(2) INFORMATION FOR SEQ ID NO:67:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

TCTCACTCCT	CGAGCCCGAA	GTTGTCCAGC	GTGGGTGTTA	TGACTAAGGT	CACGGAGCTG	60
------------	------------	------------	------------	------------	------------	----

CCCACGGAGG GGCCTAACGC CATTAGTATT CCGATCTCCG CGACCCTCGG CCCGCGCAAC 120  
CCGCTCCGCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

TCTCACTCCT CGAGGTGGTG CGGCGCTGAG CTGTGCAACT CGGTGACTAA GAAGTTTCGC 60  
CCGGGCTGGC GGGATCACGC CAATCCCTCC ACCCATCATC GTACTCCCCC GCCCAGCCAG 120  
TCCAGCCCTT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

TCTCACTCCT CGAGGTGGTG CGGCGCTGAT GACCCGTGTG GTGCCAGTCG TTGGCGGGGG 60  
GGCAACAGCT TGTTTGGTTG TGGTCTTCGT TGTAGTGCGG CGCAGAGCAC CCCGAGTGCC 120  
AGGATCCATT CCACTTCGAC CAGCTCTAGA ATCGAAGGTG CGCTAGACCT TCGAGA 176

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

TCTCACTCCT CGAGTAAGTC CGGGGAGGGG GGTGACAGTA GCAGGGGCGA GACGGGCTGG 60  
GCGAGGGTTC GGTCTCACGC CATGACTGCT GGCCGCTTTC GGTGGTACAA CCAGTTGCC 120  
TCTGATCGGT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

TCTCACTCCT	CGAGGTCGAG	CGCCAATAAT	TGCGAGTGGA	AGTCTGATTG	GATGCGCAGG	60
GCCTGTATTG	CTCGTTACGC	CAACAGTTTCG	GGCCCCGCCC	GCGCCGTCGA	CACTAAGGCC	120
GCGCCCTCTA	GAATCGAAGG	TCGCGCTAGA	CCTTCGAGA			159

(2) INFORMATION FOR SEQ ID NO:72:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

10	TCTCACTCCT	CGAGTAAGTG	GTCGTGGAGT	TCGAGGTGGG	GCTCCCCGCA	GGATAAGGTT	60
	GAGAAGACCA	GGGCGGGTTG	TGGTGGTAGT	CCCAGCAGCA	CCAATTGTCA	CCCCTACACC	120
	TTTGCCCCC	CCCCGCAAGC	CGGCTCTAGA	ATCGAAGGTC	GCGCTAGACC	TTCGAGA	177

(2) INFORMATION FOR SEQ ID NO:73:

- 15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

TCTCACTCCT	CGAGTGGGTT	CTGGGAGTTT	AGCAGGGGGC	TTTGGGATGG	GGAGAACCGT	60
AAGAGTGTCC	GGTCGGGTTG	TGGTTTTTCG	GGCTCCTCTG	CTCAGGGCCC	GTGTCCGGTC	120
ACGCCTGCCA	CCATTGACAA	ACACTCTAGA	ATCGAAGGTC	GCGCTAGACC	TTCGAGA	177

20 (2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

25	TCTCACTCCT	CGAGTGAGAG	CGGGCGGTGC	CGTAGCGTGA	GCCGGTGGAT	GACGACGTGG	60
	CAGACGCAGA	AGGGCGGTTG	TGGTTCCAAT	GTTTCCCGCG	GTTGCCCCCT	CGACCCCTCT	120
	CACCAGACCG	GGCATGCCAC	TACTTCTAGA	ATCGAAGGTC	GCGCTAGACC	TTCGAGA	177

(2) INFORMATION FOR SEQ ID NO:75:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 162 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

TCTCACTCCT	CGAGGGAGTG	GAGGTTTGCC	GGGCCGCCGT	TGGACCTGTG	GGCGGGTCCG	60
AGCTTGCCCT	CTTTTAACGC	CAGTTCCCAC	CCTCGCGCCC	TGCGCACCTA	TTGGTCCCAG	120
CGGCCCCGCT	CTAGAATCGA	AGGTCGCGCT	AGACCTTCGA	GA		162

5 (2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TCTCACTCCT	CGAGGATGGA	GGACATCAAG	AACTCGGGGT	GGAGGGACTC	TTGTAGGTGG	60
GGTGACCTGA	GGCCTGGTTG	TGGTAGCCGC	CAGTGGTACC	CCTCGAATAT	GC GTTCTAGC	120
AGAGATTACC	CCGCGGGGGG	CCACTCTAGA	ATCGAAGGTC	GCGCTAGACC	TTCGAGA	177

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

TCTCACTCCT	CGAGTCATCC	GTGGTACAGG	CATTGGAACC	ATGGTGACTT	CTCTGGTTCG	60
GGCCAGTCAC	GCCACACCCC	GCCGGAGAGC	CCCCACCCCG	GCCGCCCTAA	TGCCACCATT	120
TCTAGAATCG	AAGGTCGCGC	TAGACCTTCG	AG			152

20 (2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

TCTCACTCCT	CGAGATATAA	GCACGATATC	GGTTGCGATG	CTGGGGTTGA	CAAGAAGTCG	60
TCGTCTGTGC	GTGGTGGTTG	TGGTGCTCAT	TNGTCGCCAC	CCCGCGCCGG	CCGTGGTCTC	120
CGCGGCACGA	TGGTTAGCAG	GCTTTCTAGA	ATCGAAGGTC	GCGCTAGACC	TTCGAGA	177

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid

30



(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

5 TCTCACTCCT CGAGTCAGGG CTCCAAGCAG TGTATGCAGT ACCGCACCGG TCGTTTGACG 60  
GTGGGGTCTG AGTATGGTTG TGGTATGAAC CCCGCCCGCC ATGCCACGCC CGCTTATCCG 120  
GCGCGCCTGC TGCCACGCTA TCGCTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA 177

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TCTCACTCCT CGAGTGGGCG GACTACTAGT GAGATTTCTG GGCTCTGGGG TTGGGGTGAC 60  
GACCGGAGCG GTTATGGTTG GGGTAACACG CTCCGCCCCA ACTACATCCC TTATAGGCAG 120  
GCGACGAACA GGCATCGTTA TACGTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA 177

(2) INFORMATION FOR SEQ ID NO:81:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 162 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

20 TCTCACTCCT CGAGGTGGAA TTGGACTGTC TTGCCCCGCA CTGGCGGCCA TTACTGGACG 60  
CGTTTCGACGG ACTATCACGC CATTAAACAT CACAGGCCGA GCATCCCCCA CCAGCATCCG 120  
ACCCCTATCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

TCTCACTCCT CGAGTTGGTC GTCGTGGAAT TGGAGCTCTA AGACTACTCG TCTGGGCGAC 60  
AGGGCGACTC GGGAGGGTTG TGGTCCCAGC CAGTCTGATG GCTGTCCTTA TAACGGCCGC 120  
CTTACGACCG TCAAGCCTCG CACGTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA 177

30 (2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 156 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

TCTCACTCCT	CGAGTGGTAG	TTTGAACGCA	TGGCAACCGC	GGTCATGGGT	GGGGGGCGCG	60
TTCCGGTCAC	ACGCCAACAA	TAAGTTGAAC	CCCAAGCCCA	CCATGGTTAC	TNGTCACCCT	120
ACCTCTAGAA	TCGAAGGTCG	CGCTAGACCT	TCGAGA			156

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 178 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

TCTCACTCCT	CGAGGTATTC	GGGTTTGTCC	CCGCGGGACA	ACGGTCCCGC	TTGTAGTCAG	60
GAGGCTACCT	TGGAGGGTTG	TGGTGCGCAG	AGGCTGATGT	CCACCCGTCG	CAAGGGCCGC	120
AACTCCCGCC	CCGGGTGGAC	GCTCTCTAGA	ATCGAAGGTC	GCGCTAGACC	CTTCGAGA	178

15 (2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 162 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TCTCACTCCT	CGAGCGTGGG	GAATGATAAG	ACTAGCAGGC	CGGTTTCCTT	CTACGGGCGC	60
GTTAGTGATC	TGTGGAACGC	CAGCTTGATG	CCGAAGCGTA	CTCCCAGCTC	GAAGCGCCAC	120
GATGATGGCT	CTAGAATCGA	AGGTCGCGCT	AGACCTTCGA	GA		162

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 162 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

TCTCACTCCT	CGAGTACTCC	CCCCAGTAGG	GAGGCGTATA	GTAGGCCCTA	TAGTGTCGAT	60
AGCGATTTCG	ATACGAACGC	CAAGCACAGC	TCCCACAACC	GCCGTNTGCG	GACGCGCAGC	120
CGCCCGAACT	CTAGAATCGA	AGGTCGCGCT	AGACCTTCGA	GA		162

30

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 159 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TCTCACTCCT	CGAGATGGCC	TAGTGTGGGT	TACAAGGGTA	ATGGCAGTGA	CACTATTGAT	60
GTTCACAGCA	ATGACGCCAG	TACTAAGAGG	TCCCTCATCT	ATAACCACCG	CCGCCCCNTC	120
TTTCCCTCTA	GAATCGAAGG	TCGCGCTAGA	CCTTCGAGA			159

(2) INFORMATION FOR SEQ ID NO:88:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 162 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

15	TCTCACTCCT	CGAGAACGTT	TGAGAACGAC	GGGCTGGGCG	TCGGCCGGTC	TATTCAGAAG	60
	AAGTCGGATA	GGTGGTACGC	CAGCCACAAC	ATTCGTAGCC	ATTTCGCGTC	CATGTCTCCC	120
	GCTGGTAAGT	CTAGAATCGA	AGGTCGCGCT	AGACCTTCGA	GA		162

(2) INFORMATION FOR SEQ ID NO:89:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 160 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

TCTCACTCCT	CGAGCTATTG	TCGGGTTAAG	GGTGGTGGGG	AGGGGGGGCA	TACGGATTCC	60
AATCTGGCTA	GGTCGGGTTG	TGGTAAGGTG	GCCAGGACCA	GCAGGCTTCA	GCATATCAAC	120
CCGCGCGCTA	CCCCCCCCTC	CCGGTCTAGA	ATCGAAGGTC			160

(2) INFORMATION FOR SEQ ID NO:90:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 162 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

30	TCTCACTCCT	CGAGTTGGAC	TCGGTGGGGC	AAGCACANTC	ATGGGGGGTT	TGTGAACAAG	60
----	------------	------------	------------	------------	------------	------------	----

TCTCCCCCTG GGAAGAACGC CACGAGCCCC TACACCGACG CCCAGCTGCC CAGTGATCAG 120  
GGTCCTCCCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TCTCACTCCT CGAGTCAGGT TGATTCGTTT CGTAATAGCT TTCGGTGGTA TGAGCCGAGC 60  
AGGGCTCTGT GCCATGGTTG TGGTAAGCGC GACACCTCCA CCACTCGTAT CCACAATAGC 120  
CCCAGCGACT CCTATCCTAC ACGCTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA 177

10 (2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TCTCACTCCT CGAGCTTTTT GCGGTTCCAG AGTCCGAGGT TCGAGGATTA CAGTAGGACG 60  
ATCTNTCGGT TGCGCAACGC CACGAACCCG AGTAATGTCT CCGATGCGCA CAATAACCGG 120  
GCCTTGGCCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 162 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

25 TCTCACTCCT CGAGGAGCAT CACCGACGGG GGCATCAATG AGGTGGACCT GAGTAGTGTG 60  
TCGAACGTTT TTGAGAACGC CAACTCGCAT AGGGCCTACA GGAAGCATCG CCCGACCTTG 120  
AAGCGTCCTT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

TCTCACTCCT	CGAGTTCGAA	GGTGAGCAGC	CCGAGGGGATC	CGACGGTCCC	GCGGAAGGGC	60
GGCAATGTTG	ATTATGGTTG	TGGTCACAGG	TCTTCCGCC	GGATGCCTAC	CTCCGCTCTG	120
TCGTCGATCA	CGAAGTGCTA	CACTTCTAGA	ATCGAAGGTC	GCGCTAGACC	TTCGAGA	177

(2) INFORMATION FOR SEQ ID NO:95:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 177 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

10	TCTCACTCCT	CGAGAGCCAG	TANGCAGGGC	GGCCGGGGTG	TTGCCCCTGA	GTTTGGGGCG	60
	AGCGTTTTTG	GTNGTGGTTG	TGGTAGCGCC	ACTTATTACA	CGAACTCCAC	CAGCTGCAAG	120
	GATGCTATGG	GCCACAATA	CTCGTCTAGA	ATCGAAGGTC	GCGNTAGACC	TTCGAGA	177

(2) INFORMATION FOR SEQ ID NO:96:

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 162 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

TCTCACTCCT	CGAGATGGTG	CGAGAAGCAC	AAGTTTACGG	CTGCGCGTTG	CAGCGCGGGG	60
GCGGGTTTTG	AGAGGGANGC	CAGCCGTCCG	CCCCAGCCTG	CCCACCGGGA	TAATACCAAC	120
CGTAATGCNT	NTAGAATCGA	AGGTCGCGCT	AGACCTTCGA	GA		162

20 (2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 162 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

25	TCTCACTCCT	CGAGTTTTCA	GGTGTACCCG	GACCATGGTC	TGGAGAGGCA	TGCTTTGGAC	60
	GGGACGGGTC	CGCTTTACGC	CATGCCCGGC	CGCTGGATTA	GGGCGCGTCC	GCAGAACAGG	120
	GACCGCCAGT	CTAGAATCGA	AGGTCGCGCT	AGACCTTCGA	GA		162

(2) INFORMATION FOR SEQ ID NO:98:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 159 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

TCTCACTCCT	CGAGCAGGTG	TACGGACAAC	GAGCAGTGCC	CCGATACCGG	GANTAGGTCT	60
CGTTCCGTTA	GTAACGCCAG	GTA CTTTTCG	AGCAGGTTGC	TCAAGACTCA	CGCCCCCAT	120
CGCCCTTCTA	GAATCGAAGG	TCGCGCTAGA	CCTTCGAGA			159

5 (2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TCTCACTCCT	CGAGTGCCAG	GGATAGCGGG	CCTGCGGAGG	ATGGGTCCCCG	CGCCGTCCGG	60
TTGAACGGGG	TTGAGAACGC	CAACACTAGG	AAGTCCTCCC	GCAGTAACCC	GCGGGGTAGG	120
CGCCATCCCT	CTAGAATCGA	AGGTCGCGCT	AGACCTTCGA	GA		162

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

TCTCACTCCT	CGAGTTCCGC	CGATGCGGAG	AAGTGTGCGG	GCAGTCTGTT	GTGGTGGGGT	60
AGGCAGAAC	ACTCCGGTTG	TGGTTCGCCC	ACGAAGAAGC	ATCTGAAGCA	CCGCAATCGC	120
AGTCAGACCT	CCTCTTCGTC	CCACTCTAGA	ATCGAAGGTC	GCGCTAGACC	TTCGAGA	177

20 (2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TCTCACTCCT	CGAGACCGAA	GAACGTGGCC	GATGCTTATT	CGTCTCAGGA	CGGGGCGGCG	60
GCCGAGGAGA	CGTCTCACGC	CAGTAATGCC	GCGCGGAAGT	CCCCTAAGCA	CAAGCCCTTG	120
AGGCGGCCTT	CTAGAATCGA	AGGTCGCGCT	AGACCTTCGA	GA		162

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid

30

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

5 TCTCACTCCT CGAGAGGCAG TACGGGGACG GCCGGCGGCG AGCGTTCCGG GGTGCTCAAC 60  
CTGCACACCA GGGATAACGC CAGCGGCAGC GGTTTCAAAC CGTGGTACCC TTCGAATCGG 120  
GGTCACAAGT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 162 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

TCTCACTCCT CGAGGTGGGG GTGGGAGAGG AGTCCGTCCG ACTACGATTC TGATATGGAC 60  
TTGGGGGCGA GGAGGTACGC CACCCGCACC CACCGCGCGC CCCCTCGCGT CTTGAAGGCT 120  
CCCCTGCCCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO:104:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

20 TCTCACTCCT CGAGGCACTG GAAGTGCAGG GGCTCTCAGG CTGCCTACGG GGACAAGGAT 60  
ATCGGGAGGT CCAGGGGTTG TGGTTCCATT ACAAAGAATA AACTAATCA CGCCCATCCT 120  
AGCCACGGCG CCGTTGCTAA GATCTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA 177

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 162 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

TCTCACTCCT CGAGCCGCGA GGAGGCGAAC TGGGACGGCT ATAAGAGGGA GATGAGCCAC 60  
CGGAGTCGCT TTTGGGACGC CACCCACCTG TCCGCCCCTC GCCGCCCCGC TAACTCTGGT 120  
GACCCTAACT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

30 (2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 177 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TCTCACTCNT	CGAGAGAGTT	CGCGGAGAGG	AGGTTGTGGG	GGTGTGATGA	CCTGAGTTGG	60
CGTCTCGACG	CGGAGGGTTG	TGGTCCCACT	CCGAGCAATC	GGGCCGTCAA	GCATCGCAAG	120
CCCCGCCCCAC	GCTCCCCCGC	ACTCTCTAGA	ATCGAAGGTC	GCGCTAGACC	TTCGAGA	177

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 177 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

TCTCACTCNT	NGAGTGATCA	CGCGTTGGGG	ACGAATCTGA	GGTCTGACAA	TGCCAAGGAG	60
CCGGGTGATT	ACAAGTGTG	TGGTAACGGG	AACTCTACCG	GGCGAAAGGT	TTTTAACCGT	120
15 AGGCGCCCCCT	CGCCATCCC	CANTTCTAGA	ATCGAAGGTC	GCGCTAGACC	TTCGAGA	177

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 177 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

TCTCACTCCT	CGAGGCATAT	TTCTGAGTAT	AGCTTTGCGA	ATTCCCCTT	GATGGGTGGC	60
GAGTCCAAGC	GGAAGGGTTG	TGGTATTAAC	GGCTCCTTTT	CTCCCCTTG	TCCCCGCTCC	120
CCCACCCAG	CCTTCCGCCG	CACCTCTAGA	ATCGAAGGTC	GCGCTAGACC	TTCGAGA	177

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 158 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

TCTCACTCCT	CGAGCCGGGA	GAGCGGGATG	TGGGGTAGTT	GGTGGCGTGG	TCACAGGTTG	60
30 AATTCCACGG	GGGGTAACGC	CAACATGAAT	GCTAGTCTGC	CCCCCGACCC	CCCTGTTTCC	120
ACTCCGTCTA	GAATCGAAGG	TCGCGCTAGA	CCTTCGAG			158



(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

	Met	Gly	Met	Ser	Lys	Ser	His	Ser	Phe	Phe	Gly	Tyr	Pro	Leu	Ser	Ile
	1				5					10					15	
	Phe	Phe	Ile	Val	Val	Asn	Glu	Phe	Cys	Glu	Arg	Phe	Ser	Tyr	Tyr	Gly
				20					25					30		
	Met	Arg	Ala	Ile	Leu	Ile	Leu	Tyr	Phe	Thr	Asn	Phe	Ile	Ser	Trp	Asp
			35					40					45			
10	Asp	Asn	Leu	Ser	Thr	Ala	Ile	Tyr	His	Thr	Phe	Val	Ala	Leu	Cys	Tyr
		50					55					60				
	Leu	Thr	Pro	Ile	Leu	Gly	Ala	Leu	Ile	Ala	Asp	Ser	Trp	Leu	Gly	Lys
	65					70					75				80	
	Phe	Lys	Thr	Ile	Val	Ser	Leu	Ser	Ile	Val	Tyr	Thr	Ile	Gly	Gln	Ala
				85						90				95		
	Val	Thr	Ser	Val	Ser	Ser	Ile	Asn	Asp	Leu	Thr	Asp	His	Asn	His	Asp
				100					105					110		
	Gly	Thr	Pro	Asp	Ser	Leu	Pro	Val	His	Val	Val	Leu	Ser	Leu	Ile	Gly
			115					120						125		
15	Leu	Ala	Leu	Ile	Ala	Leu	Gly	Thr	Gly	Gly	Ile	Lys	Pro	Cys	Val	Ser
		130					135						140			
	Ala	Phe	Gly	Gly	Asp	Gln	Phe	Glu	Glu	Gly	Gln	Glu	Lys	Gln	Arg	Asn
	145					150					155				160	
	Arg	Phe	Phe	Ser	Ile	Phe	Tyr	Leu	Ala	Ile	Asn	Ala	Gly	Ser	Leu	Leu
				165						170					175	
	Ser	Thr	Ile	Ile	Thr	Pro	Met	Leu	Arg	Val	Gln	Gln	Cys	Gly	Ile	His
				180					185					190		
	Ser	Lys	Gln	Ala	Cys	Tyr	Pro	Leu	Ala	Phe	Gly	Val	Pro	Ala	Ala	Leu
			195					200					205			
20	Met	Ala	Val	Ala	Leu	Ile	Val	Phe	Val	Leu	Gly	Ser	Gly	Met	Tyr	Lys
		210					215						220			
	Lys	Phe	Lys	Pro	Gln	Gly	Asn	Ile	Met	Gly	Lys	Val	Ala	Lys	Cys	Ile
	225					230					235				240	
	Gly	Phe	Ala	Ile	Lys	Asn	Arg	Phe	Arg	His	Arg	Ser	Lys	Ala	Phe	Pro
				245						250					255	
	Lys	Arg	Glu	His	Trp	Leu	Asp	Trp	Ala	Lys	Glu	Lys	Tyr	Asp	Glu	Arg
			260						265					270		
	Leu	Ile	Ser	Gln	Ile	Lys	Met	Val	Thr	Arg	Val	Met	Phe	Leu	Tyr	Ile
			275					280					285			
25	Pro	Leu	Pro	Met	Phe	Trp	Ala	Leu	Phe	Asp	Gln	Gln	Gly	Ser	Arg	Trp
		290					295					300				
	Thr	Leu	Gln	Ala	Thr	Thr	Met	Ser	Gly	Lys	Ile	Gly	Ala	Leu	Glu	Ile
	305					310					315				320	
	Gln	Pro	Asp	Gln	Met	Gln	Thr	Val	Asn	Ala	Ile	Leu	Ile	Val	Ile	Met
				325						330					335	
	Val	Pro	Ile	Phe	Asp	Ala	Val	Leu	Tyr	Pro	Leu	Ile	Ala	Lys	Cys	Gly
			340						345					350		
	Phe	Asn	Phe	Thr	Ser	Leu	Lys	Lys	Met	Ala	Val	Gly	Met	Val	Leu	Ala
			355					360					365			
30	Ser	Met	Ala	Phe	Val	Val	Ala	Ala	Ile	Val	Gln	Val	Glu	Ile	Asp	Lys
		370					375					380				
	Thr	Leu	Pro	Val	Phe	Pro	Lys	Gly	Asn	Glu	Val	Gln	Ile	Lys	Val	Leu

	385				390				395				400
	Asn	Ile	Gly	Asn	Asn	Thr	Met	Asn	Ile	Ser	Leu	Pro	Gly
					405					410			Glu
	Thr	Leu	Gly	Pro	Met	Ser	Gln	Thr	Asn	Ala	Phe	Met	Thr
				420					425				Phe
	Asn	Lys	Leu	Thr	Arg	Ile	Asn	Ile	Ser	Ser	Pro	Gly	Ser
				435					440				Pro
	Ala	Val	Thr	Asp	Asp	Phe	Lys	Gln	Gly	Gln	Arg	His	Thr
5							455					460	Leu
	Trp	Ala	Pro	Asn	His	Tyr	Gln	Val	Val	Lys	Asp	Gly	Leu
	465					470					475		Asn
	Pro	Glu	Lys	Gly	Glu	Asn	Gly	Ile	Arg	Phe	Val	Asn	Thr
					485					490			Phe
	Leu	Ile	Thr	Ile	Thr	Met	Ser	Gly	Lys	Val	Tyr	Ala	Asn
				500					505				Ile
	Tyr	Asn	Ala	Ser	Thr	Tyr	Gln	Phe	Phe	Pro	Ser	Gly	Ile
				515				520					Lys
	Thr	Ile	Ser	Ser	Thr	Glu	Ile	Pro	Pro	Gln	Cys	Gln	Pro
10								535				540	Asn
	Thr	Phe	Tyr	Leu	Glu	Phe	Gly	Ser	Ala	Tyr	Thr	Tyr	Ile
	545					550					555		Val
	Lys	Asn	Asp	Ser	Cys	Pro	Glu	Val	Lys	Val	Phe	Glu	Asp
				565						570			Ile
	Asn	Thr	Val	Asn	Met	Ala	Leu	Gln	Ile	Pro	Gln	Tyr	Phe
				580					585				Leu
	Cys	Gly	Glu	Val	Val	Phe	Ser	Val	Thr	Gly	Leu	Glu	Phe
				595				600					Ser
	Gln	Ala	Pro	Ser	Asn	Met	Lys	Ser	Val	Leu	Gln	Ala	Gly
15							615					620	Trp
	Thr	Val	Ala	Val	Gly	Asn	Ile	Ile	Val	Leu	Ile	Val	Ala
	625					630					635		Gly
	Gln	Phe	Ser	Lys	Gln	Trp	Ala	Glu	Tyr	Ile	Leu	Phe	Ala
				645						650			Ala
	Leu	Val	Val	Cys	Val	Val	Phe	Ala	Ile	Met	Ala	Arg	Phe
				660					665				Tyr
	Ile	Asn	Pro	Ala	Glu	Ile	Glu	Ala	Gln	Phe	Asp	Glu	Asp
				675				680				685	Glu
	Asn	Arg	Leu	Glu	Lys	Ser	Asn	Pro	Tyr	Phe	Met	Ser	Gly
20							695					700	Ala
	Gln	Lys	Gln	Met									Asn
	705												Ser

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TCCGGACTCT CATAAGCGCC GG

22

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

5 ACAACGGGCC AGAAAGAGCG AG 22

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

ACACCACCCC AATCGGAGCT AC 22

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

TCAGAATCCG TGCACTGGCC AA 22

(2) INFORMATION FOR SEQ ID NO:115:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

25 GCCCTATTCA TACCACCGGA GT 22

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:  
CATCAGTCCT ACCGCCGAAA AG 22

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:  
CGTATAGCTA TTGTGAGCGA TG 22

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:  
ACGCGCGGAA CGAGCAGTAC CA 22

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:  
CCATAATGAT CCCCCTCACT AT 22

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:  
AGACACCCCT TAGCCGTCGT AG 22

(2) INFORMATION FOR SEQ ID NO:121:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:  
 AGCTCCGTGA CCTTAGTCAT AA 22

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:  
 TGCACAGCTC AGCGCCGCAC CA 22

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:  
 20 ACGGGTCATC AGCGCCGCAC CA 22

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:  
 TGTCACCCCC CTCCCCGAC TT 22

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ACTCGCAATT ATTGGCGCTC GA 22

(2) INFORMATION FOR SEQ ID NO:126:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

10 GTCTTCTCAA CCTTATCCTG CG 22

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

AAAGCCCCCT GCTAAACTCC CA 22

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

20 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CTGCGTCTGC CACGTCGTCA TC 22

(2) INFORMATION FOR SEQ ID NO:129:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

30 GTTAAAAGAG GGCAAGCTCG GA 22

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:  
 CCGAGTTCTT GATGTCCTCC AT 22

(2) INFORMATION FOR SEQ ID NO:131:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:  
 TCCAATGCCT GTACCACGGA TG 22

15 (2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:  
 TCGCAACCGA TATCGTGCTT AT 22

(2) INFORMATION FOR SEQ ID NO:133:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:  
 TGCATACACT GCTTGGAGCC CT 22

(2) INFORMATION FOR SEQ ID NO:134:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

5 GAAATCTCAC TAGTAGTCCG CC 22

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GCGGGCAAGA CAGTCCAATT CC 22

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
15 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GAGCTCCAAT TCCACGACGA CC 22

(2) INFORMATION FOR SEQ ID NO:137:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

25 GGTGCCATG CGTTCAAAC AC 22

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:  
TCCCGCGGGG ACAAACCCGA AT 22

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:  
CTGCTAGTCT TATCATTCCC CA 22

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:  
CTATCGACAC TATAGGGCCT AC 22

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:  
TACCCTTGTA ACCCACAATA GG 22

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:  
TTCTTCTGAA TAGACCGGCC GA 22

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:  
 CCACCACCCT TAACCCGACA AT 22

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:  
 AGGGGGAGAC TTGTTCAACA AC 22

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:  
 CGGCTCATAC CACCGAAAGC TA 22

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:  
 ATCGTCCTAC TGTAATCCTC GA 22

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

GACACACTAC TCAGGTCCAC CT 22

(2) INFORMATION FOR SEQ ID NO:148:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

CCATAATCAA CATTGCCGCC CT 22

10 (2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

CAAAACGCTC GCCCCAAACT CA 22

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GTAAACTTGT GCTTCTCGCA CC 22

(2) INFORMATION FOR SEQ ID NO:151:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

30 CCATGGTCCG GGTACACCTG AA 22

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GTTACTAACG GAACGAGACC TA 22

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 10 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

TGTTGGCGTT CTCAACCCCG TT 22

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ACAACCGGAG TTGTTCTGCC TA 22

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

TAAGCATCGG CCACGTTCTT CG 22

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:  
 30 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

5 TTATCCCTGG TGTGCAGGTT GA 22

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

TATCAGAATC GTAGTCGGAC GG 22

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

CTTTGTAATG GAACCACAAC CC 22

(2) INFORMATION FOR SEQ ID NO:159:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

25 CGGTGGCTCA TCTCCCTCTT AT 22

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:  
 ATCAGACTGG CTGGGACCAC AA 22

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:  
 CACAACCTCC TCTCCGCGAA CT 22

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:  
 AGATTCGTCC CCAACGCGTG AT 22

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:  
 GGGAATTCGC AAAGCTATAC TC 22

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:  
 CCCC GTG GAA TTCAACCTGT GA 22

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:  
 GTCGTCTTTC CAGACGT 17

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:  
 CTTGCATGCC TGCAGGTCGA C 21

(2) INFORMATION FOR SEQ ID NO:167:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

20 Arg Ile Ala Gly Leu Pro Trp Tyr Arg Cys Arg Thr Val Ala Phe Glu  
 1 5 10 15  
 Thr Gly Met Gln Asn Thr Gln Leu Cys Ser Thr Ile Val Gln Leu Ser  
 20 25 30  
 Phe Thr Pro Glu Glu  
 35

(2) INFORMATION FOR SEQ ID NO:168:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 44 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

30 Arg Glu Phe Ala Glu Arg Arg Leu Trp Gly Cys Asp Asp Leu Ser Trp  
 1 5 10 15  
 Arg Leu Asp Ala Glu Gly Cys Gly Pro Thr Pro Ser Asn Arg Ala Val  
 20 25 30

Lys His Arg Lys Pro Arg Pro Arg Ser Pro Ala Leu  
35 40

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

5  
10  
15  
20  
25  
30  
35  
40

Ser Gly Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe  
1 5 10 15  
Arg Glu Leu Arg Asp Arg Trp Tyr Ala Thr Ser His His Thr Arg Pro  
20 25 30  
Thr Pro Gln Leu Pro Arg Gly Pro Asn  
35 40

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

15  
20

Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp  
1 5 10 15  
Ser Asp Ser Asp  
20

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

25  
30

Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp  
1 5 10 15  
Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser His Asn  
20 25

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids  
(B) TYPE: amino acid



(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

5 Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg Ser  
1 5 10 15  
Arg Pro Asn

(2) INFORMATION FOR SEQ ID NO:173:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

Thr Asn Ala Lys His Ser Ser His Asn  
1 5

(2) INFORMATION FOR SEQ ID NO:174:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

20 Ser Ser His Asn Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn  
1 5 10

(2) INFORMATION FOR SEQ ID NO:175:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn  
1 5 10

(2) INFORMATION FOR SEQ ID NO:176:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 708 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

5	Met	Gly	Met	Ser	Lys	Ser	His	Ser	Phe	Phe	Gly	Tyr	Pro	Leu	Ser	Ile	1	5	10	15
	Phe	Phe	Ile	Val	Val	Asn	Glu	Phe	Cys	Glu	Arg	Phe	Ser	Tyr	Tyr	Gly	20	25	30	
	Met	Arg	Ala	Ile	Leu	Ile	Leu	Tyr	Phe	Thr	Asn	Phe	Ile	Ser	Trp	Asp	35	40	45	
	Asp	Asn	Leu	Ser	Thr	Ala	Ile	Tyr	His	Thr	Phe	Val	Ala	Leu	Cys	Tyr	50	55	60	
	Leu	Thr	Pro	Ile	Leu	Gly	Ala	Leu	Ile	Ala	Asp	Ser	Trp	Leu	Gly	Lys	65	70	75	80
10	Phe	Lys	Thr	Ile	Val	Ser	Leu	Ser	Ile	Val	Tyr	Thr	Ile	Gly	Gln	Ala	85	90	95	
	Val	Thr	Ser	Val	Ser	Ser	Ile	Asn	Asp	Leu	Thr	Asp	His	Asn	His	Asp	100	105	110	
	Gly	Thr	Pro	Asp	Ser	Leu	Pro	Val	His	Val	Val	Leu	Ser	Leu	Ile	Gly	115	120	125	
	Leu	Ala	Leu	Ile	Ala	Leu	Gly	Thr	Gly	Gly	Ile	Lys	Pro	Cys	Val	Ser	130	135	140	
	Ala	Phe	Gly	Gly	Asp	Gln	Phe	Glu	Glu	Gly	Gln	Glu	Lys	Gln	Arg	Asn	145	150	155	160
15	Arg	Phe	Phe	Ser	Ile	Phe	Tyr	Leu	Ala	Ile	Asn	Ala	Gly	Ser	Leu	Leu	165	170	175	
	Ser	Thr	Ile	Ile	Thr	Pro	Met	Leu	Arg	Val	Gln	Gln	Cys	Gly	Ile	His	180	185	190	
	Ser	Lys	Gln	Ala	Cys	Tyr	Pro	Leu	Ala	Phe	Gly	Val	Pro	Ala	Ala	Leu	195	200	205	
	Met	Ala	Val	Ala	Leu	Ile	Val	Phe	Val	Leu	Gly	Ser	Gly	Met	Tyr	Lys	210	215	220	
	Lys	Phe	Lys	Pro	Gln	Gly	Asn	Ile	Met	Gly	Lys	Val	Ala	Lys	Cys	Ile	225	230	235	240
20	Gly	Phe	Ala	Ile	Lys	Asn	Arg	Phe	Arg	His	Arg	Ser	Lys	Ala	Phe	Pro	245	250	255	
	Lys	Arg	Glu	His	Trp	Leu	Asp	Trp	Ala	Lys	Glu	Lys	Tyr	Asp	Glu	Arg	260	265	270	
	Leu	Ile	Ser	Gln	Ile	Lys	Met	Val	Thr	Arg	Val	Met	Phe	Leu	Tyr	Ile	275	280	285	
	Pro	Leu	Pro	Met	Phe	Trp	Ala	Leu	Phe	Asp	Gln	Gln	Gly	Ser	Arg	Trp	290	295	300	
	Thr	Leu	Gln	Ala	Thr	Thr	Met	Ser	Gly	Lys	Ile	Gly	Ala	Leu	Glu	Ile	305	310	315	320
25	Gln	Pro	Asp	Gln	Met	Gln	Thr	Val	Asn	Ala	Ile	Leu	Ile	Val	Ile	Met	325	330	335	
	Val	Pro	Ile	Phe	Asp	Ala	Val	Leu	Tyr	Pro	Leu	Ile	Ala	Lys	Cys	Gly	340	345	350	
	Phe	Asn	Phe	Thr	Ser	Leu	Lys	Lys	Met	Ala	Val	Gly	Met	Val	Leu	Ala	355	360	365	
	Ser	Met	Ala	Phe	Val	Val	Ala	Ala	Ile	Val	Gln	Val	Glu	Ile	Asp	Lys	370	375	380	
	Thr	Leu	Pro	Val	Phe	Pro	Lys	Gly	Asn	Glu	Val	Gln	Ile	Lys	Val	Leu	385	390	395	400
30	Asn	Ile	Gly	Asn	Asn	Thr	Met	Asn	Ile	Ser	Leu	Pro	Gly	Glu	Met	Val	405	410	415	
	Thr	Leu	Gly	Pro	Met	Ser	Gln	Thr	Asn	Ala	Phe	Met	Thr	Phe	Asp	Val				

			420				425				430					
	Asn	Lys	Leu	Thr	Arg	Ile	Asn	Ile	Ser	Ser	Pro	Gly	Ser	Pro	Val	Thr
			435					440					445			
	Ala	Val	Thr	Asp	Asp	Phe	Lys	Gln	Gly	Gln	Arg	His	Thr	Leu	Leu	Val
			450				455					460				
	Trp	Ala	Pro	Asn	His	Tyr	Gln	Val	Val	Lys	Asp	Gly	Leu	Asn	Gln	Lys
	465					470					475				480	
	Pro	Glu	Lys	Gly	Glu	Asn	Gly	Ile	Arg	Phe	Val	Asn	Thr	Phe	Asn	Glu
5					485					490				495		
	Leu	Ile	Thr	Ile	Thr	Met	Ser	Gly	Lys	Val	Tyr	Ala	Asn	Ile	Ser	Ser
				500					505					510		
	Tyr	Asn	Ala	Ser	Thr	Tyr	Gln	Phe	Phe	Pro	Ser	Gly	Ile	Lys	Gly	Phe
			515					520					525			
	Thr	Ile	Ser	Ser	Thr	Glu	Ile	Pro	Pro	Gln	Cys	Gln	Pro	Asn	Phe	Asn
			530				535					540				
	Thr	Phe	Tyr	Leu	Glu	Phe	Gly	Ser	Ala	Tyr	Thr	Tyr	Ile	Val	Gln	Arg
	545				550					555					560	
	Lys	Asn	Asp	Ser	Cys	Pro	Glu	Val	Lys	Val	Phe	Glu	Asp	Ile	Ser	Ala
10					565					570				575		
	Asn	Thr	Val	Asn	Met	Ala	Leu	Gln	Ile	Pro	Gln	Tyr	Phe	Leu	Leu	Thr
				580					585					590		
	Cys	Gly	Glu	Val	Val	Phe	Ser	Val	Thr	Gly	Leu	Glu	Phe	Ser	Tyr	Ser
			595					600					605			
	Gln	Ala	Pro	Ser	Asn	Met	Lys	Ser	Val	Leu	Gln	Ala	Gly	Trp	Leu	Leu
			610				615					620				
	Thr	Val	Ala	Val	Gly	Asn	Ile	Ile	Val	Leu	Ile	Val	Ala	Gly	Ala	Gly
	625				630					635					640	
	Gln	Phe	Ser	Lys	Gln	Trp	Ala	Glu	Tyr	Ile	Leu	Phe	Ala	Ala	Leu	Leu
15					645					650				655		
	Leu	Val	Val	Cys	Val	Val	Phe	Ala	Ile	Met	Ala	Arg	Phe	Tyr	Thr	Tyr
				660					665					670		
	Ile	Asn	Pro	Ala	Glu	Ile	Glu	Ala	Gln	Phe	Asp	Glu	Asp	Glu	Lys	Lys
			675				680					685				
	Asn	Arg	Leu	Glu	Lys	Ser	Asn	Pro	Tyr	Phe	Met	Ser	Gly	Ala	Asn	Ser
	690						695					700				
	Gln	Lys	Gln	Met												
	705															

20 (2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3345 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

25 (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 88...2583  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GAATTCCGTC	TCGACCACTG	AATGGAAGAA	AAGGACTTTT	AACCACCATT	TTGTGACTTA	60
CAGAAAGGAA	TTTGAATAAA	GAAAACT	ATG ATA	CTT CAG	GCC CAT CTT CAC TCC	114
			Met	Ile	Leu Gln Ala His	
			1		5	

30

	CTG	TGT	CTT	CTT	ATG	CTT	TAT	TTG	GCA	ACT	GGA	TAT	GGC	CAA	GAG	GGG	162
	Leu	Cys	Leu	Leu	Met	Leu	Tyr	Leu	Ala	Thr	Gly	Tyr	Gly	Gln	Glu	Gly	
	10					15					20					25	
	AAG	TTT	AGT	GGA	CCC	CTG	AAA	CCC	ATG	ACA	TTT	TCT	ATT	TAT	GAA	GGC	210
	Lys	Phe	Ser	Gly	Pro	Leu	Lys	Pro	Met	Thr	Phe	Ser	Ile	Tyr	Glu	Gly	
					30					35					40		
5	CAA	GAA	CCG	AGT	CAA	ATT	ATA	TTC	CAG	TTT	AAG	GCC	AAT	CCT	CCT	GCT	258
	Gln	Glu	Pro	Ser	Gln	Ile	Ile	Phe	Gln	Phe	Lys	Ala	Asn	Pro	Pro	Ala	
				45					50					55			
	GTG	ACT	TTT	GAA	CTA	ACT	GGG	GAG	ACA	GAC	AAC	ATA	TTT	GTG	ATA	GAA	306
	Val	Thr	Phe	Glu	Leu	Thr	Gly	Glu	Thr	Asp	Asn	Ile	Phe	Val	Ile	Glu	
			60					65					70				
	CGG	GAG	GGA	CTT	CTG	TAT	TAC	AAC	AGA	GCC	TTG	GAC	AGG	GAA	ACA	AGA	354
	Arg	Glu	Gly	Leu	Leu	Tyr	Tyr	Asn	Arg	Ala	Leu	Asp	Arg	Glu	Thr	Arg	
10		75					80					85					
	TCT	ACT	CAC	AAT	CTC	CAG	GTT	GCA	GCC	CTG	GAC	GCT	AAT	GGA	ATT	ATA	402
	Ser	Thr	His	Asn	Leu	Gln	Val	Ala	Ala	Leu	Asp	Ala	Asn	Gly	Ile	Ile	
	90					95					100					105	
	GTG	GAG	GGT	CCA	GTC	CCT	ATC	ACC	ATA	GAA	GTG	AAG	GAC	ATC	AAC	GAC	450
	Val	Glu	Gly	Pro	Val	Pro	Ile	Thr	Ile	Glu	Val	Lys	Asp	Ile	Asn	Asp	
					110					115					120		
15	AAT	CGA	CCC	ACG	TTT	CTC	CAG	TCA	AAG	TAC	GAA	GGC	TCA	GTA	AGG	CAG	498
	Asn	Arg	Pro	Thr	Phe	Leu	Gln	Ser	Lys	Tyr	Glu	Gly	Ser	Val	Arg	Gln	
				125					130					135			
	AAC	TCT	CGC	CCA	GGA	AAG	CCC	TTC	TTG	TAT	GTC	AAT	GCC	ACA	GAC	CTG	546
	Asn	Ser	Arg	Pro	Gly	Lys	Pro	Phe	Leu	Tyr	Val	Asn	Ala	Thr	Asp	Leu	
			140					145					150				
	GAT	GAT	CCG	GCC	ACT	CCC	AAT	GGC	CAG	CTT	TAT	TAC	CAG	ATT	GTC	ATC	594
	Asp	Asp	Pro	Ala	Thr	Pro	Asn	Gly	Gln	Leu	Tyr	Tyr	Gln	Ile	Val	Ile	
20		155					160					165					
	CAG	CTT	CCC	ATG	ATC	AAC	AAT	GTC	ATG	TAC	TTT	CAG	ATC	AAC	AAC	AAA	642
	Gln	Leu	Pro	Met	Ile	Asn	Asn	Val	Met	Tyr	Phe	Gln	Ile	Asn	Asn	Lys	
	170					175					180					185	
	ACG	GGA	GCC	ATC	TCT	CTT	ACC	CGA	GAG	GGA	TCT	CAG	GAA	TTG	AAT	CCT	690
	Thr	Gly	Ala	Ile	Ser	Leu	Thr	Arg	Glu	Gly	Ser	Gln	Glu	Leu	Asn	Pro	
					190					195					200		
25	GCT	AAG	AAT	CCT	TCC	TAT	AAT	CTG	GTG	ATC	TCA	GTG	AAG	GAC	ATG	GGA	738
	Ala	Lys	Asn	Pro	Ser	Tyr	Asn	Leu	Val	Ile	Ser	Val	Lys	Asp	Met	Gly	
				205					210					215			
	GGC	CAG	AGT	GAG	AAT	TCC	TTC	AGT	GAT	ACC	ACA	TCT	GTG	GAT	ATC	ATA	786
	Gly	Gln	Ser	Glu	Asn	Ser	Phe	Ser	Asp	Thr	Thr	Ser	Val	Asp	Ile	Ile	
			220					225					230				
	GTG	ACA	GAG	AAT	ATT	TGG	AAA	GCA	CCA	AAA	CCT	GTG	GAG	ATG	GTG	GAA	834
	Val	Thr	Glu	Asn	Ile	Trp	Lys	Ala	Pro	Lys	Pro	Val	Glu	Met	Val	Glu	
30		235					240					245					
	AAC	TCA	ACT	GAT	CCT	CAC	CCC	ATC	AAA	ATC	ACT	CAG	GTG	CGG	TGG	AAT	882

	Asn 250	Ser	Thr	Asp	Pro	His 255	Pro	Ile	Lys	Ile	Thr 260	Gln	Val	Arg	Trp	Asn 265	
	GAT Asp	CCC Pro	GGT Gly	GCA Ala	CAA Gln	TAT Tyr	TCC Ser	TTA Leu	GTT Val	GAC Asp	AAA Lys	GAG Glu	AAG Lys	CTG Leu	CCA Pro	AGA Arg	930
5	TTC Phe	CCA Pro	TTT Phe	TCA Ser	ATT Ile	GAC Asp	CAG Gln	GAA Glu	GGA Gly	GAT Asp	ATT Ile	TAC Tyr	GTG Val	ACT Thr	CAG Gln	CCC Pro	978
	TTG Leu	GAC Asp	CGA Arg	GAA Glu	GAA Glu	AAG Lys	GAT Asp	GCA Ala	TAT Tyr	GTT Val	TTT Phe	TAT Tyr	GCA Ala	GTT Val	GCA Ala	AAG Lys	1026
	GAT Asp	GAG Glu	TAC Tyr	GGA Gly	AAA Lys	CCA Pro	CTT Leu	TCA Ser	TAT Tyr	CCG Pro	CTG Leu	GAA Glu	ATT Ile	CAT His	GTA Val	AAA Lys	1074
10	GTT Val	AAA Lys	GAT Asp	ATT Ile	AAT Asn	GAT Asp	AAT Asn	CCA Pro	CCT Pro	ACA Thr	TGT Cys	CCG Pro	TCA Ser	CCA Pro	GTA Val	ACC Thr	1122
	GTA Val	TTT Phe	GAG Glu	GTC Val	CAG Gln	GAG Glu	AAT Asn	GAA Glu	CGA Arg	CTG Leu	GGT Gly	AAC Asn	AGT Ser	ATC Ile	GGG Gly	ACC Thr	1170
15	CTT Leu	ACT Thr	GCA Ala	CAT His	GAC Asp	AGG Arg	GAT Asp	GAA Glu	GAA Glu	AAT Asn	ACT Thr	GCC Ala	AAC Asn	AGT Ser	TTT Phe	CTA Leu	1218
	AAC Asn	TAC Tyr	AGG Arg	ATT Ile	GTG Val	GAG Glu	CAA Gln	ACT Thr	CCC Pro	AAA Lys	CTT Leu	CCC Pro	ATG Met	GAT Asp	GGA Gly	CTC Leu	1266
	TTC Phe	CTA Leu	ATC Ile	CAA Gln	ACC Thr	TAT Tyr	GCT Ala	GGA Gly	ATG Met	TTA Leu	CAG Gln	TTA Leu	GCT Ala	AAA Lys	CAG Gln	TCC Ser	1314
20	TTG Leu	AAG Lys	AAG Lys	CAA Gln	GAT Asp	ACT Thr	CCT Pro	CAG Gln	TAC Tyr	AAC Asn	TTA Leu	ACG Thr	ATA Ile	GAG Glu	GTG Val	TCT Ser	1362
	GAC Asp	AAA Lys	GAT Asp	TTC Phe	AAG Lys	ACC Thr	CTT Leu	TGT Cys	TTT Phe	GTG Val	CAA Gln	ATC Ile	AAC Asn	GTT Val	ATT Ile	GAT Asp	1410
25	ATC Ile	AAT Asn	GAT Asp	CAG Gln	ATC Ile	CCC Pro	ATC Ile	TTT Phe	GAA Glu	AAA Lys	TCA Ser	GAT Asp	TAT Tyr	GGA Gly	AAC Asn	CTG Leu	1458
	ACT Thr	CTT Leu	GCT Ala	GAA Glu	GAC Asp	ACA Thr	AAC Asn	ATT Ile	GGG Gly	TCC Ser	ACC Thr	ATC Ile	TTA Leu	ACC Thr	ATC Ile	CAG Gln	1506
	GCC Ala	ACT Thr	GAT Asp	GCT Ala	GAT Asp	GAG Glu	CCA Pro	TTT Phe	ACT Thr	GGG Gly	AGT Ser	TCT Ser	AAA Lys	ATT Ile	CTG Leu	TAT Tyr	1554
30	CAT His	ATC Ile	ATA Ile	AAG Lys	GGA Gly	GAC Asp	AGT Ser	GAG Glu	GGA Gly	CGC Arg	CTG Leu	GGG Gly	GTT Val	GAC Asp	ACA Thr	GAT Asp	1602

	490					495					500					505					
	CCC Pro	CAT His	ACC Thr	AAC Asn	ACC Thr 510	GGA Gly	TAT Tyr	GTC Val	ATA Ile	ATT Ile 515	AAA Lys	AAG Lys	CCT Pro	CTT Leu	GAT Asp 520	TTT Phe	1650				
5	GAA Glu	ACA Thr	GCA Ala	GCT Ala 525	GTT Val	TCC Ser	AAC Asn	ATT Ile	GTG Val 530	TTC Phe	AAA Lys	GCA Ala	GAA Glu	AAT Asn 535	CCT Pro	GAG Glu	1698				
	CCT Pro	CTA Leu	GTG Val 540	TTT Phe	GGT Gly	GTG Val	AAG Lys	TAC Tyr 545	AAT Asn	GCA Ala	AGT Ser	TCT Ser	TTT Phe 550	GCC Ala	AAG Lys	TTC Phe	1746				
	ACG Thr	CTT Leu 555	ATT Ile	GTG Val	ACA Thr	GAT Asp	GTG Val 560	AAT Asn	GAA Glu	GCA Ala	CCT Pro	CAA Gln 565	TTT Phe	TCC Ser	CAA Gln	CAC His	1794				
10	GTA Val 570	TTC Phe	CAA Gln	GCG Ala	AAA Lys	GTC Val 575	AGT Ser	GAG Glu	GAT Asp	GTA Val	GCT Ala 580	ATA Ile	GGC Gly	ACT Thr	AAA Lys	GTG Val 585	1842				
	GGC Gly	AAT Asn	GTG Val	ACT Thr	GCC Ala 590	AAG Lys	GAT Asp	CCA Pro	GAA Glu	GGT Gly 595	CTG Leu	GAC Asp	ATA Ile	AGC Ser	TAT Tyr 600	TCA Ser	1890				
15	CTG Leu	AGG Arg	GGA Gly	GAC Asp 605	ACA Thr	AGA Arg	GGT Gly	TGG Trp	CTT Leu 610	AAA Lys	ATT Ile	GAC Asp	CAC His	GTG Val 615	ACT Thr	GGT Gly	1938				
	GAG Glu	ATC Ile	TTT Phe 620	AGT Ser	GTG Val	GCT Ala	CCA Pro	TTG Leu 625	GAC Asp	AGA Arg	GAA Glu	GCC Ala	GGA Gly 630	AGT Ser	CCA Pro	TAT Tyr	1986				
20	CGG Arg	GTA Val 635	CAA Gln	GTG Val	GTG Val	GCC Ala	ACA Thr 640	GAA Glu	GTA Val	GGG Gly	GGG Gly	TCT Ser 645	TCC Ser	TTA Leu	AGC Ser	TCT Ser	2034				
	GTG Val 650	TCA Ser	GAG Glu	TTC Phe	CAC His	CTG Leu 655	ATC Ile	CTT Leu	ATG Met	GAT Asp	GTG Val 660	AAT Asn	GAC Asp	AAC Asn	CCT Pro	CCC Pro 665	2082				
	AGG Arg	CTA Leu	GCC Ala	AAG Lys	GAC Asp 670	TAC Tyr	ACG Thr	GGC Gly	TTG Leu	TTC Phe 675	TTC Phe	TGC Cys	CAT His	CCC Pro	CTC Leu 680	AGT Ser	2130				
25	GCA Ala	CCT Pro	GGA Gly	AGT Ser 685	CTC Leu	ATT Ile	TTC Phe	GAG Glu	GCT Ala 690	ACT Thr	GAT Asp	GAT Asp	GAT Asp	CAG Gln 695	CAC His	TTA Leu	2178				
	TTT Phe	CGG Arg	GGT Gly 700	CCC Pro	CAT His	TTT Phe	ACA Thr	TTT Phe 705	TCC Ser	CTC Leu	GGC Gly	AGT Ser	GGA Gly 710	AGC Ser	TTA Leu	CAA Gln	2226				
30	AAC Asn	GAC Asp 715	TGG Trp	GAA Glu	GTT Val	TCC Ser	AAA Lys 720	ATC Ile	AAT Asn	GGT Gly	ACT Thr	CAT His	GCC Ala	CGA Arg	CTG Leu	TCT Ser	2274				
	ACC Thr 730	AGG Arg	CAC His	ACA Thr	GAC Asp	TTT Phe 735	GAG Glu	GAG Glu	AGG Arg	GCG Ala	TAT Tyr 740	GTC Val	GTC Val	TTG Leu	ATC Ile	CGC Arg 745	2322				

	ATC AAT GAT GGG GGT CGG CCA CCC TTG GAA GGC ATT GTT TCT TTA CCA	2370
	Ile Asn Asp Gly Gly Arg Pro Pro Leu Glu Gly Ile Val Ser Leu Pro	
	750 755 760	
	GTT ACA TTC TGC AGT TGT GTG GAA GGA AGT TGT TTC CGG CCA GCA GGT	2418
	Val Thr Phe Cys Ser Cys Val Glu Gly Ser Cys Phe Arg Pro Ala Gly	
	765 770 775	
5	CAC CAG ACT GGG ATA CCC ACT GTG GGC ATG GCA GTT GGT ATA CTG CTG	2466
	His Gln Thr Gly Ile Pro Thr Val Gly Met Ala Val Gly Ile Leu Leu	
	780 785 790	
	ACC ACC CTT CTG GTG ATT GGT ATA ATT TTA GCA GTT GTG TTT ATC CGC	2514
	Thr Thr Leu Leu Val Ile Gly Ile Ile Leu Ala Val Val Phe Ile Arg	
	795 800 805	
	ATA AAG AAG GAT AAA GGC AAA GAT AAT GTT GAA AGT GCT CAA GCA TCT	2562
	Ile Lys Lys Asp Lys Gly Lys Asp Asn Val Glu Ser Ala Gln Ala Ser	
10	810 815 820 825	
	GAA GTC AAA CCT CTG AGA AGC TGAATTTGAA AAGGAATGTT TGAATTTATA TAGC	2617
	Glu Val Lys Pro Leu Arg Ser	
	830	
	AAGTGCTATT TCAGCAACAA CCATCTCATC CTATTACTTT TCATCTAACG TGCATTATAA	2677
	TTTTTTAAAC AGATATTTCC TCTTGTCCTT TAATATTTGC TAAATATTTT TTTTTTGAGG	2737
	TGGAGTCTTG CTCTGTCGCC CAGGCTGGAG TACAGTGGTG TGATCCCAGC TCACTGCAAC	2797
	CTCCGCCTCC TGGGTTTACA TGATTCTCCT GCCTCAGCTT CCTAAGTAGC TGGGTTTACA	2857
15	GGCACCCACC ACCATGCCCA GCTAATTTTT GTATTTTTTAA TAGAGACGGG GTTTCGCCAT	2917
	TTGGCCAGGC TGGTCTTGAA CTCCTGACGT CAAGTGATCT GCCTGCCTTG GTCTCCCAAT	2977
	ACAGGCATGA ACCACTGCAC CCACCTACTT AGATATTTCA TGTGCTATAG ACATTAGAGA	3037
	GATTTTTTCAT TTTTCCATGA CATTTTTTCT CTCTGCAAAT GGCTTAGCTA CTTGTGTTTT	3097
	TCCCTTTTGG GGCAAGACAG ACTCATTAAA TATTCTGTAC ATTTTTTCTT TATCAAGGAG	3157
	ATATATCAGT GTTGTCCTCAT AGAACTGCCT GGATTCCATT TATGTTTTTT CTGATTCCAT	3217
	CCTGTGTCCC CTTTCATCCT GACTCCTTTG GTATTTTCACT GAATTTCAA CATTTGTGTCAG	3277
	AGAAGAAAAA AGTGAGGACT CAGGAAAAAT AAATAAATAA AAGAACAGCC TTTTGCGGCC	3337
	GCGAATTC	3345

20 (2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 832 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

	Met Ile Leu Gln Ala His Leu His Ser Leu Cys Leu Leu Met Leu Tyr	
	1 5 10 15	
	Leu Ala Thr Gly Tyr Gly Gln Glu Gly Lys Phe Ser Gly Pro Leu Lys	
	20 25 30	
	Pro Met Thr Phe Ser Ile Tyr Glu Gly Gln Glu Pro Ser Gln Ile Ile	
	35 40 45	
	Phe Gln Phe Lys Ala Asn Pro Pro Ala Val Thr Phe Glu Leu Thr Gly	
	50 55 60	
30	Glu Thr Asp Asn Ile Phe Val Ile Glu Arg Glu Gly Leu Leu Tyr Tyr	
	65 70 75 80	
	Asn Arg Ala Leu Asp Arg Glu Thr Arg Ser Thr His Asn Leu Gln Val	

				85				90				95				
	Ala	Ala	Leu	Asp	Ala	Asn	Gly	Ile	Ile	Val	Glu	Gly	Pro	Val	Pro	Ile
				100					105					110		
	Thr	Ile	Glu	Val	Lys	Asp	Ile	Asn	Asp	Asn	Arg	Pro	Thr	Phe	Leu	Gln
			115					120					125			
	Ser	Lys	Tyr	Glu	Gly	Ser	Val	Arg	Gln	Asn	Ser	Arg	Pro	Gly	Lys	Pro
			130				135					140				
5	Phe	Leu	Tyr	Val	Asn	Ala	Thr	Asp	Leu	Asp	Asp	Pro	Ala	Thr	Pro	Asn
	145				150					155					160	
	Gly	Gln	Leu	Tyr	Tyr	Gln	Ile	Val	Ile	Gln	Leu	Pro	Met	Ile	Asn	Asn
				165						170				175		
	Val	Met	Tyr	Phe	Gln	Ile	Asn	Asn	Lys	Thr	Gly	Ala	Ile	Ser	Leu	Thr
			180					185						190		
	Arg	Glu	Gly	Ser	Gln	Glu	Leu	Asn	Pro	Ala	Lys	Asn	Pro	Ser	Tyr	Asn
			195					200					205			
	Leu	Val	Ile	Ser	Val	Lys	Asp	Met	Gly	Gly	Gln	Ser	Glu	Asn	Ser	Phe
		210					215					220				
10	Ser	Asp	Thr	Thr	Ser	Val	Asp	Ile	Ile	Val	Thr	Glu	Asn	Ile	Trp	Lys
	225				230						235				240	
	Ala	Pro	Lys	Pro	Val	Glu	Met	Val	Glu	Asn	Ser	Thr	Asp	Pro	His	Pro
				245					250					255		
	Ile	Lys	Ile	Thr	Gln	Val	Arg	Trp	Asn	Asp	Pro	Gly	Ala	Gln	Tyr	Ser
			260					265						270		
	Leu	Val	Asp	Lys	Glu	Lys	Leu	Pro	Arg	Phe	Pro	Phe	Ser	Ile	Asp	Gln
			275				280					285				
	Glu	Gly	Asp	Ile	Tyr	Val	Thr	Gln	Pro	Leu	Asp	Arg	Glu	Glu	Lys	Asp
		290					295				300					
15	Ala	Tyr	Val	Phe	Tyr	Ala	Val	Ala	Lys	Asp	Glu	Tyr	Gly	Lys	Pro	Leu
	305				310					315					320	
	Ser	Tyr	Pro	Leu	Glu	Ile	His	Val	Lys	Val	Lys	Asp	Ile	Asn	Asp	Asn
				325					330					335		
	Pro	Pro	Thr	Cys	Pro	Ser	Pro	Val	Thr	Val	Phe	Glu	Val	Gln	Glu	Asn
			340					345						350		
	Glu	Arg	Leu	Gly	Asn	Ser	Ile	Gly	Thr	Leu	Thr	Ala	His	Asp	Arg	Asp
		355					360					365				
	Glu	Glu	Asn	Thr	Ala	Asn	Ser	Phe	Leu	Asn	Tyr	Arg	Ile	Val	Glu	Gln
		370				375					380					
20	Thr	Pro	Lys	Leu	Pro	Met	Asp	Gly	Leu	Phe	Leu	Ile	Gln	Thr	Tyr	Ala
	385				390					395					400	
	Gly	Met	Leu	Gln	Leu	Ala	Lys	Gln	Ser	Leu	Lys	Lys	Gln	Asp	Thr	Pro
				405					410					415		
	Gln	Tyr	Asn	Leu	Thr	Ile	Glu	Val	Ser	Asp	Lys	Asp	Phe	Lys	Thr	Leu
			420					425					430			
	Cys	Phe	Val	Gln	Ile	Asn	Val	Ile	Asp	Ile	Asn	Asp	Gln	Ile	Pro	Ile
		435					440					445				
	Phe	Glu	Lys	Ser	Asp	Tyr	Gly	Asn	Leu	Thr	Leu	Ala	Glu	Asp	Thr	Asn
		450				455					460					
25	Ile	Gly	Ser	Thr	Ile	Leu	Thr	Ile	Gln	Ala	Thr	Asp	Ala	Asp	Glu	Pro
	465				470					475					480	
	Phe	Thr	Gly	Ser	Ser	Lys	Ile	Leu	Tyr	His	Ile	Ile	Lys	Gly	Asp	Ser
				485					490					495		
	Glu	Gly	Arg	Leu	Gly	Val	Asp	Thr	Asp	Pro	His	Thr	Asn	Thr	Gly	Tyr
			500					505					510			
	Val	Ile	Ile	Lys	Lys	Pro	Leu	Asp	Phe	Glu	Thr	Ala	Ala	Val	Ser	Asn
			515				520					525				
	Ile	Val	Phe	Lys	Ala	Glu	Asn	Pro	Glu	Pro	Leu	Val	Phe	Gly	Val	Lys
		530				535					540					
30	Tyr	Asn	Ala	Ser	Ser	Phe	Ala	Lys	Phe	Thr	Leu	Ile	Val	Thr	Asp	Val
	545				550					555					560	
	Asn	Glu	Ala	Pro	Gln	Phe	Ser	Gln	His	Val	Phe	Gln	Ala	Lys	Val	Ser
				565					570					575		



	Glu	Asp	Val	Ala	Ile	Gly	Thr	Lys	Val	Gly	Asn	Val	Thr	Ala	Lys	Asp
				580					585					590		
	Pro	Glu	Gly	Leu	Asp	Ile	Ser	Tyr	Ser	Leu	Arg	Gly	Asp	Thr	Arg	Gly
			595					600					605			
	Trp	Leu	Lys	Ile	Asp	His	Val	Thr	Gly	Glu	Ile	Phe	Ser	Val	Ala	Pro
		610				615						620				
	Leu	Asp	Arg	Glu	Ala	Gly	Ser	Pro	Tyr	Arg	Val	Gln	Val	Val	Ala	Thr
		625				630					635					640
5	Glu	Val	Gly	Gly	Ser	Leu	Ser	Ser	Val	Ser	Glu	Phe	His	Leu	Ile	
				645					650					655		
	Leu	Met	Asp	Val	Asn	Asp	Asn	Pro	Pro	Arg	Leu	Ala	Lys	Asp	Tyr	Thr
				660				665						670		
	Gly	Leu	Phe	Phe	Cys	His	Pro	Leu	Ser	Ala	Pro	Gly	Ser	Leu	Ile	Phe
			675				680						685			
	Glu	Ala	Thr	Asp	Asp	Asp	Gln	His	Leu	Phe	Arg	Gly	Pro	His	Phe	Thr
		690				695						700				
	Phe	Ser	Leu	Gly	Ser	Gly	Ser	Leu	Gln	Asn	Asp	Trp	Glu	Val	Ser	Lys
		705			710						715					720
10	Ile	Asn	Gly	Thr	His	Ala	Arg	Leu	Ser	Thr	Arg	His	Thr	Asp	Phe	Glu
				725						730				735		
	Glu	Arg	Ala	Tyr	Val	Val	Leu	Ile	Arg	Ile	Asn	Asp	Gly	Gly	Arg	Pro
				740					745					750		
	Pro	Leu	Glu	Gly	Ile	Val	Ser	Leu	Pro	Val	Thr	Phe	Cys	Ser	Cys	Val
			755				760						765			
	Glu	Gly	Ser	Cys	Phe	Arg	Pro	Ala	Gly	His	Gln	Thr	Gly	Ile	Pro	Thr
			770				775					780				
	Val	Gly	Met	Ala	Val	Gly	Ile	Leu	Leu	Thr	Thr	Leu	Leu	Val	Ile	Gly
		785				790					795					800
15	Ile	Ile	Leu	Ala	Val	Phe	Ile	Arg	Ile	Lys	Lys	Asp	Lys	Gly	Lys	
				805					810					815		
	Asp	Asn	Val	Glu	Ser	Ala	Gln	Ala	Ser	Glu	Val	Lys	Pro	Leu	Arg	Ser
				820				825						830		

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1827 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

20

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

	Met	Ala	Arg	Lys	Lys	Phe	Ser	Gly	Leu	Glu	Ile	Ser	Leu	Ile	Val	Leu
	1				5					10					15	
	Phe	Val	Ile	Val	Thr	Ile	Ile	Ala	Ile	Ala	Leu	Ile	Val	Val	Leu	Ala
				20					25					30		
25	Thr	Lys	Thr	Pro	Ala	Val	Asp	Glu	Ile	Ser	Asp	Ser	Thr	Ser	Thr	Pro
			35					40					45			
	Ala	Thr	Thr	Arg	Val	Thr	Thr	Asn	Pro	Ser	Asp	Ser	Gly	Lys	Cys	Pro
			50				55					60				
	Asn	Val	Leu	Asn	Asp	Pro	Val	Asn	Val	Arg	Ile	Asn	Cys	Ile	Pro	Glu
					70					75					80	
	Gln	Phe	Pro	Thr	Glu	Gly	Ile	Cys	Ala	Gln	Arg	Gly	Cys	Cys	Trp	Arg
				85						90					95	
	Pro	Trp	Asn	Asp	Ser	Leu	Ile	Pro	Trp	Cys	Phe	Phe	Val	Asp	Asn	His
				100					105					110		
30	Gly	Tyr	Asn	Val	Gln	Asp	Met	Thr	Thr	Thr	Ser	Ile	Gly	Val	Glu	Ala
			115					120					125			

	Lys	Leu	Asn	Arg	Ile	Pro	Ser	Pro	Thr	Leu	Phe	Gly	Asn	Asp	Ile	Asn
	130						135					140				
	Ser	Val	Leu	Phe	Thr	Thr	Gln	Asn	Gln	Thr	Pro	Asn	Arg	Phe	Arg	Phe
	145					150					155					160
	Lys	Ile	Thr	Asp	Pro	Asn	Asn	Arg	Arg	Tyr	Glu	Val	Pro	His	Gln	Tyr
				165						170					175	
	Val	Lys	Glu	Phe	Thr	Gly	Pro	Thr	Val	Ser	Asp	Thr	Leu	Tyr	Asp	Val
				180					185					190		
5	Lys	Val	Ala	Gln	Asn	Pro	Phe	Ser	Ile	Gln	Val	Ile	Arg	Lys	Ser	Asn
			195				200						205			
	Gly	Lys	Thr	Leu	Phe	Asp	Thr	Ser	Ile	Gly	Pro	Leu	Val	Tyr	Ser	Asp
	210					215					220					
	Gln	Tyr	Leu	Gln	Ile	Ser	Ala	Arg	Leu	Pro	Ser	Asp	Tyr	Ile	Tyr	Gly
	225					230					235					240
	Ile	Gly	Glu	Gln	Val	His	Lys	Arg	Phe	Arg	His	Asp	Leu	Ser	Trp	Lys
					245					250					255	
	Thr	Trp	Pro	Ile	Phe	Thr	Arg	Asp	Gln	Leu	Pro	Gly	Asp	Asn	Asn	Asn
				260					265					270		
10	Asn	Leu	Tyr	Gly	His	Gln	Thr	Phe	Phe	Met	Cys	Ile	Glu	Asp	Thr	Ser
			275					280					285			
	Gly	Lys	Ser	Phe	Gly	Val	Phe	Leu	Met	Asn	Ser	Asn	Ala	Met	Glu	Ile
	290						295					300				
	Phe	Ile	Gln	Pro	Thr	Pro	Ile	Val	Thr	Tyr	Arg	Val	Thr	Gly	Gly	Ile
	305					310					315					320
	Leu	Asp	Phe	Tyr	Ile	Leu	Leu	Gly	Asp	Thr	Pro	Glu	Gln	Val	Val	Gln
					325					330					335	
	Gln	Tyr	Gln	Gln	Leu	Val	Gly	Leu	Pro	Ala	Met	Pro	Ala	Tyr	Trp	Asn
					340				345					350		
15	Leu	Gly	Phe	Gln	Leu	Ser	Arg	Trp	Asn	Tyr	Lys	Ser	Leu	Asp	Val	Val
			355					360					365			
	Lys	Glu	Val	Val	Arg	Arg	Asn	Arg	Glu	Ala	Gly	Ile	Pro	Phe	Asp	Thr
	370						375					380				
	Gln	Val	Thr	Asp	Ile	Asp	Tyr	Met	Glu	Asp	Lys	Lys	Asp	Phe	Thr	Tyr
	385					390					395					400
	Asp	Gln	Val	Ala	Phe	Asn	Gly	Leu	Pro	Gln	Phe	Val	Gln	Asp	Leu	His
					405					410					415	
	Asp	His	Gly	Gln	Lys	Tyr	Val	Ile	Ile	Leu	Asp	Pro	Ala	Ile	Ser	Ile
					420				425					430		
20	Gly	Arg	Arg	Ala	Asn	Gly	Thr	Thr	Tyr	Ala	Thr	Tyr	Glu	Arg	Gly	Asn
			435					440					445			
	Thr	Gln	His	Val	Trp	Ile	Asn	Glu	Ser	Asp	Gly	Ser	Thr	Pro	Ile	Ile
	450						455					460				
	Gly	Glu	Val	Trp	Pro	Gly	Leu	Thr	Val	Tyr	Pro	Asp	Phe	Thr	Asn	Pro
	465					470					475					480
	Asn	Cys	Ile	Asp	Trp	Trp	Ala	Asn	Glu	Cys	Ser	Ile	Phe	His	Gln	Glu
					485					490					495	
	Val	Gln	Tyr	Asp	Gly	Leu	Trp	Ile	Asp	Met	Asn	Glu	Val	Ser	Ser	Phe
				500					505					510		
25	Ile	Gln	Gly	Ser	Thr	Lys	Gly	Cys	Asn	Val	Asn	Lys	Leu	Asn	Tyr	Pro
			515					520					525			
	Pro	Phe	Thr	Pro	Asp	Ile	Leu	Asp	Lys	Leu	Met	Tyr	Ser	Lys	Thr	Ile
	530						535					540				
	Cys	Met	Asp	Ala	Val	Gln	Asn	Trp	Gly	Lys	Gln	Tyr	Asp	Val	His	Ser
	545					550					555					560
	Leu	Tyr	Gly	Tyr	Ser	Met	Ala	Ile	Ala	Thr	Glu	Gln	Ala	Val	Gln	Lys
					565					570					575	
	Val	Phe	Pro	Asn	Lys	Arg	Ser	Phe	Ile	Leu	Thr	Arg	Ser	Thr	Phe	Ala
				580					585					590		
30	Gly	Ser	Gly	Arg	His	Ala	Ala	His	Trp	Leu	Gly	Asp	Asn	Thr	Ala	Ser
			595					600					605			
	Trp	Glu	Gln	Met	Glu	Trp	Ser	Ile	Thr	Gly	Met	Leu	Glu	Phe	Ser	Leu

	610		615		620
	Phe Gly Ile Pro Leu Val Gly Ala Asp Ile Cys Gly Phe Val Ala Glu				
	625 Thr Thr Glu Glu Leu Cys Arg Arg Trp Met Gln Leu Gly Ala Phe Tyr				
		645		650	655
	Pro Phe Ser Arg Asn His Asn Ser Asp Gly Tyr Glu His Gln Asp Pro				
		660		665	670
5	Ala Phe Phe Gly Gln Asn Ser Leu Leu Val Lys Ser Ser Arg Gln Tyr				
		675		680	685
	Leu Thr Ile Arg Tyr Thr Leu Leu Pro Phe Leu Tyr Thr Leu Phe Tyr				
		690		695	700
	Lys Ala His Val Phe Gly Glu Thr Val Ala Arg Pro Val Leu His Glu				
	705 Phe Tyr Glu Asp Thr Asn Ser Trp Ile Glu Asp Thr Glu Phe Leu Trp				
		710		715	720
		725		730	735
	Gly Pro Ala Leu Leu Ile Thr Pro Val Leu Lys Gln Gly Ala Asp Thr				
		740		745	750
10	Val Ser Ala Tyr Ile Pro Asp Ala Ile Trp Tyr Asp Tyr Glu Ser Gly				
		755		760	765
	Ala Lys Arg Pro Trp Arg Lys Gln Arg Val Asp Met Tyr Leu Pro Ala				
		770		775	780
	Asp Lys Ile Gly Leu His Leu Arg Gly Gly Tyr Ile Ile Pro Ile Gln				
	785 Glu Pro Asp Val Thr Thr Thr Ala Ser Arg Lys Asn Pro Leu Gly Leu				
		790		795	800
		805		810	815
	Ile Val Ala Leu Gly Glu Asn Asn Thr Ala Lys Gly Asp Phe Phe Trp				
		820		825	830
15	Asp Asp Gly Glu Thr Lys Asp Thr Ile Gln Asn Gly Asn Tyr Ile Leu				
		835		840	845
	Tyr Thr Phe Ser Val Ser Asn Asn Thr Leu Asp Ile Val Cys Thr His				
		850		855	860
	Ser Ser Tyr Gln Glu Gly Thr Thr Leu Ala Phe Gln Thr Val Lys Ile				
		865		870	875
	Leu Gly Leu Thr Asp Ser Val Thr Glu Val Arg Val Ala Glu Asn Asn				
		885		890	895
	Gln Pro Met Asn Ala His Ser Asn Phe Thr Tyr Asp Ala Ser Asn Gln				
		900		905	910
20	Val Leu Leu Ile Ala Asp Leu Lys Leu Asn Leu Gly Arg Asn Phe Ser				
		915		920	925
	Val Gln Trp Asn Gln Ile Phe Ser Glu Asn Glu Arg Phe Asn Cys Tyr				
		930		935	940
	Pro Asp Ala Asp Leu Ala Thr Glu Gln Lys Cys Thr Gln Arg Gly Cys				
		945		950	955
	Val Trp Arg Thr Gly Ser Ser Leu Ser Lys Ala Pro Glu Cys Tyr Phe				
		965		970	975
	Pro Arg Gln Asp Asn Ser Tyr Ser Val Asn Ser Ala Arg Tyr Ser Ser				
		980		985	990
25	Met Gly Ile Thr Ala Asp Leu Gln Leu Asn Thr Ala Asn Ala Arg Ile				
		995		1000	1005
	Lys Leu Pro Ser Asp Pro Ile Ser Thr Leu Arg Val Glu Val Lys Tyr				
		1010		1015	1020
	His Lys Asn Asp Met Leu Gln Phe Lys Ile Tyr Asp Pro Gln Lys Lys				
		1025		1030	1035
	Arg Tyr Glu Val Pro Val Pro Leu Asn Ile Pro Thr Thr Pro Ile Ser				
		1045		1050	1055
	Thr Tyr Glu Asp Arg Leu Tyr Asp Val Glu Ile Lys Glu Asn Pro Phe				
		1060		1065	1070
	Gly Ile Gln Ile Arg Arg Arg Ser Gly Arg Val Ile Trp Asp Ser				
		1075		1080	1085
30	Trp Leu Pro Gly Phe Ala Phe Asn Asp Gln Phe Ile Gln Ile Ser Thr				
		1090		1095	1100

Arg Leu Pro Ser Glu Tyr Ile Tyr Gly Phe Gly Glu Val Glu His Thr  
 105 1110 1115 1120  
 Ala Phe Lys Arg Asp Leu Asn Trp Asn Thr Trp Gly Met Phe Thr Arg  
 1125 1130 1135  
 Asp Gln Pro Pro Gly Tyr Lys Leu Asn Ser Tyr Gly Phe His Pro Tyr  
 1140 1145 1150  
 Tyr Met Ala Leu Glu Glu Glu Gly Asn Ala His Gly Val Phe Leu Leu  
 1155 1160 1165  
 5 Asn Ser Asn Ala Met Asp Val Thr Phe Gln Pro Thr Pro Ala Leu Thr  
 1170 1175 1180  
 Tyr Arg Thr Val Gly Gly Ile Leu Asp Phe Tyr Met Phe Leu Gly Pro  
 185 1190 1195 1200  
 Thr Pro Gln Val Ala Thr Lys Gln Tyr His Glu Val Ile Gly His Pro  
 1205 1210 1215  
 Val Met Pro Ala Tyr Trp Ala Leu Gly Phe Gln Leu Cys Arg Tyr Gly  
 1220 1225 1230  
 Tyr Ala Asn Thr Ser Glu Val Arg Glu Leu Tyr Asp Ala Met Val Ala  
 1235 1240 1245  
 10 Ala Asn Ile Pro Tyr Asp Val Gln Tyr Thr Asp Ile Asp Tyr Met Glu  
 1250 1255 1260  
 Arg Gln Leu Asp Phe Thr Ile Gly Glu Ala Phe Gln Asp Leu Pro Gln  
 265 1270 1275 1280  
 Phe Val Asp Lys Ile Arg Gly Glu Gly Met Arg Tyr Ile Ile Ile Leu  
 1285 1290 1295  
 Asp Pro Ala Ile Ser Gly Asn Glu Thr Lys Thr Tyr Pro Ala Phe Glu  
 1300 1305 1310  
 Arg Gly Gln Gln Asn Asp Val Phe Val Lys Trp Pro Asn Thr Asn Asp  
 1315 1320 1325  
 15 Ile Cys Trp Ala Lys Val Trp Pro Asp Leu Pro Asn Ile Thr Ile Asp  
 1330 1335 1340  
 Lys Thr Leu Thr Glu Asp Glu Ala Val Asn Ala Ser Arg Ala His Val  
 345 1350 1355 1360  
 Ala Phe Pro Asp Phe Phe Arg Thr Ser Thr Ala Glu Trp Trp Ala Arg  
 1365 1370 1375  
 Glu Ile Val Asp Phe Tyr Asn Glu Lys Met Lys Phe Asp Gly Leu Trp  
 1380 1385 1390  
 Ile Asp Met Asn Glu Pro Ser Ser Phe Val Asn Gly Thr Thr Thr Asn  
 1395 1400 1405  
 20 Gln Cys Arg Asn Asp Glu Leu Asn Tyr Pro Pro Tyr Phe Pro Glu Leu  
 1410 1415 1420  
 Thr Lys Arg Thr Asp Gly Leu His Phe Arg Thr Ile Cys Met Glu Ala  
 425 1430 1435 1440  
 Glu Gln Ile Leu Ser Asp Gly Thr Ser Val Leu His Tyr Asp Val His  
 1445 1450 1455  
 Asn Leu Tyr Gly Trp Ser Gln Met Lys Pro Thr His Asp Ala Leu Gln  
 1460 1465 1470  
 Lys Thr Thr Gly Lys Arg Gly Ile Val Ile Ser Arg Ser Thr Tyr Pro  
 1475 1480 1485  
 25 Thr Ser Gly Arg Trp Gly Gly His Trp Leu Gly Asp Asn Tyr Ala Arg  
 1490 1495 1500  
 Trp Asp Asn Met Asp Lys Ser Ile Ile Gly Met Met Glu Phe Ser Leu  
 505 1510 1515 1520  
 Phe Gly Ile Ser Tyr Thr Gly Ala Asp Ile Cys Gly Phe Phe Asn Asn  
 1525 1530 1535  
 Ser Glu Tyr His Leu Cys Thr Arg Trp Met Gln Leu Gly Ala Phe Tyr  
 1540 1545 1550  
 Pro Tyr Ser Arg Asn His Asn Ile Ala Asn Thr Arg Arg Gln Asp Pro  
 1555 1560 1565  
 30 Ala Ser Trp Asn Glu Thr Phe Ala Glu Met Ser Arg Asn Ile Leu Asn  
 1570 1575 1580  
 Ile Arg Tyr Thr Leu Leu Pro Tyr Phe Tyr Thr Gln Met His Glu Ile



	CCA	GGC	AGC	TCA	ACA	GAC	AAC	CTG	AAG	CAC	AGC	ACC	AGG	GGC	ATC	CTT	200
	Pro	Gly	Ser	Ser	Thr	Asp	Asn	Leu	Lys	His	Ser	Thr	Arg	Gly	Ile	Leu	
				40					45					50			
	GGC	TCC	CAG	GAG	CCC	GAC	TTC	AAG	GGC	GTC	CAG	CCC	TAT	GCG	GGG	ATG	248
	Gly	Ser	Gln	Glu	Pro	Asp	Phe	Lys	Gly	Val	Gln	Pro	Tyr	Ala	Gly	Met	
			55					60					65				
5	CCC	AAG	GAG	GTG	CTG	TTC	CAG	TTC	TCT	GGC	CAG	GCC	CGC	TAC	CGC	ATA	296
	Pro	Lys	Glu	Val	Leu	Phe	Gln	Phe	Ser	Gly	Gln	Ala	Arg	Tyr	Arg	Ile	
		70					75					80					
	CCT	CGG	GAG	ATC	CTC	TTC	TGG	CTC	ACA	GTG	GCT	TCT	GTG	CTG	GTG	CTC	344
	Pro	Arg	Glu	Ile	Leu	Phe	Trp	Leu	Thr	Val	Ala	Ser	Val	Leu	Val	Leu	
	85					90					95					100	
	ATC	GCG	GCC	ACC	ATA	GCC	ATC	ATT	GCC	CTC	TCT	CCA	AAG	TGC	CTA	GAC	392
	Ile	Ala	Ala	Thr	Ile	Ala	Ile	Ile	Ala	Leu	Ser	Pro	Lys	Cys	Leu	Asp	
10					105				110						115		
	TGG	TGG	CAG	GAG	GGG	CCC	ATG	TAC	CAG	ATC	TAC	CCA	AGG	TCT	TTC	AAG	440
	Trp	Trp	Gln	Glu	Gly	Pro	Met	Tyr	Gln	Ile	Tyr	Pro	Arg	Ser	Phe	Lys	
				120					125					130			
	GAC	AGT	AAC	AAG	GAT	GGG	AAC	GGA	GAT	CTG	AAA	GGT	ATT	CAA	GAT	AAA	488
	Asp	Ser	Asn	Lys	Asp	Gly	Asn	Gly	Asp	Leu	Lys	Gly	Ile	Gln	Asp	Lys	
			135					140					145				
15	CTG	GAC	TAC	ATC	ACA	GCT	TTA	AAT	ATA	AAA	ACT	GTT	TGG	ATT	ACT	TCA	536
	Leu	Asp	Tyr	Ile	Thr	Ala	Leu	Asn	Ile	Lys	Thr	Val	Trp	Ile	Thr	Ser	
		150					155					160					
	TTT	TAT	AAA	TCG	TCC	CTT	AAA	GAT	TTC	AGA	TAT	GGT	GTT	GAA	GAT	TTC	584
	Phe	Tyr	Lys	Ser	Ser	Leu	Lys	Asp	Phe	Arg	Tyr	Gly	Val	Glu	Asp	Phe	
	165					170					175					180	
	CGG	GAA	GTT	GAT	CCC	ATT	TTT	GGA	ACG	ATG	GAA	GAT	TTT	GAG	AAT	CTG	632
	Arg	Glu	Val	Asp	Pro	Ile	Phe	Gly	Thr	Met	Glu	Asp	Phe	Glu	Asn	Leu	
20					185					190				195			
	GTT	GCA	GCC	ATA	CAT	GAT	AAA	GGT	TTA	AAA	TTA	ATC	ATC	GAT	TTC	ATA	680
	Val	Ala	Ala	Ile	His	Asp	Lys	Gly	Leu	Lys	Leu	Ile	Ile	Asp	Phe	Ile	
				200					205					210			
	CCA	AAC	CAC	ACG	AGT	GAT	AAA	CAT	ATT	TGG	TTT	CAA	TTG	AGT	CGG	ACA	728
	Pro	Asn	His	Thr	Ser	Asp	Lys	His	Ile	Trp	Phe	Gln	Leu	Ser	Arg	Thr	
			215					220					225				
25	CGG	ACA	GGA	AAA	TAT	ACT	GAT	TAT	TAT	ATC	TGG	CAT	GAC	TGT	ACC	CAT	776
	Arg	Thr	Gly	Lys	Tyr	Thr	Asp	Tyr	Tyr	Ile	Trp	His	Asp	Cys	Thr	His	
		230					235					240					
	GAA	AAT	GGC	AAA	ACC	ATT	CCA	CCC	AAC	AAC	TGG	TTA	AGT	GTG	TAT	GGA	824
	Glu	Asn	Gly	Lys	Thr	Ile	Pro	Pro	Asn	Asn	Trp	Leu	Ser	Val	Tyr	Gly	
	245					250					255					260	
	AAC	TCC	AGT	TGG	CAC	TTT	GAC	GAA	GTG	CGA	AAC	CAA	TGT	TAT	TTT	CAT	872
	Asn	Ser	Ser	Trp	His	Phe	Asp	Glu	Val	Arg	Asn	Gln	Cys	Tyr	Phe	His	
					265					270					275		
30	CAG	TTT	ATG	AAA	GAG	CAA	CCT	GAT	TTA	AAT	TTC	CGC	AAT	CCT	GAT	GTT	920

	Gln	Phe	Met	Lys	Glu	Gln	Pro	Asp	Leu	Asn	Phe	Arg	Asn	Pro	Asp	Val	
				280					285					290			
	CAA	GAA	GAA	ATA	AAA	GAA	ATT	TTA	CGG	TTC	TGG	CTC	ACA	AAG	GGT	GTT	968
	Gln	Glu	Glu	Ile	Lys	Glu	Ile	Leu	Arg	Phe	Trp	Leu	Thr	Lys	Gly	Val	
			295					300					305				
5	GAT	GGT	TTT	AGT	TTG	GAT	GCT	GTT	AAA	TTC	CTC	CTA	GAA	GCA	AAG	CAC	1016
	Asp	Gly	Phe	Ser	Leu	Asp	Ala	Val	Lys	Phe	Leu	Leu	Glu	Ala	Lys	His	
		310					315					320					
	CTG	AGA	GAT	GAG	ATC	CAA	GTA	AAT	AAG	ACC	CAA	ATC	CCG	GAC	ACG	GTC	1064
	Leu	Arg	Asp	Glu	Ile	Gln	Val	Asn	Lys	Thr	Gln	Ile	Pro	Asp	Thr	Val	
						330					335					340	
	ACA	CAA	TAC	TCG	GAG	CTG	TAC	CAT	GAC	TTC	ACC	ACC	ACG	CAG	GTG	GGA	1112
	Thr	Gln	Tyr	Ser	Glu	Leu	Tyr	His	Asp	Phe	Thr	Thr	Thr	Gln	Val	Gly	
					345					350					355		
10	ATG	CAC	GAC	ATT	GTC	CGC	AGC	TTC	CGG	CAG	ACC	ATG	GAC	CAA	TAC	AGC	1160
	Met	His	Asp	Ile	Val	Arg	Ser	Phe	Arg	Gln	Thr	Met	Asp	Gln	Tyr	Ser	
				360					365					370			
	ACG	GAG	CCC	GGC	AGA	TAC	AGG	TTC	ATG	GGG	ACT	GAA	GCC	TAT	GCA	GAG	1208
	Thr	Glu	Pro	Gly	Arg	Tyr	Arg	Phe	Met	Gly	Thr	Glu	Ala	Tyr	Ala	Glu	
			375					380					385				
	AGT	ATT	GAC	AGG	ACC	GTG	ATG	TAC	TAT	GGA	TTG	CCA	TTT	ATC	CAA	GAA	1256
15	Ser	Ile	Asp	Arg	Thr	Val	Met	Tyr	Tyr	Gly	Leu	Pro	Phe	Ile	Gln	Glu	
		390					395					400					
	GCT	GAT	TTT	CCC	TTC	AAC	AAT	TAC	CTC	AGC	ATG	CTA	GAC	ACT	GTT	TCT	1304
	Ala	Asp	Phe	Pro	Phe	Asn	Asn	Tyr	Leu	Ser	Met	Leu	Asp	Thr	Val	Ser	
		405				410					415					420	
	GGG	AAC	AGC	GTG	TAT	GAG	GTT	ATC	ACA	TCC	TGG	ATG	GAA	AAC	ATG	CCA	1352
	Gly	Asn	Ser	Val	Tyr	Glu	Val	Ile	Thr	Ser	Trp	Met	Glu	Asn	Met	Pro	
				425						430					435		
20	GAA	GGA	AAA	TGG	CCT	AAC	TGG	ATG	ATT	GGT	GGA	CCA	GAC	AGT	TCA	CGG	1400
	Glu	Gly	Lys	Trp	Pro	Asn	Trp	Met	Ile	Gly	Gly	Pro	Asp	Ser	Ser	Arg	
				440					445					450			
	CTG	ACT	TCG	CGT	TTG	GGG	AAT	CAG	TAT	GTC	AAC	GTG	ATG	AAC	ATG	CTT	1448
	Leu	Thr	Ser	Arg	Leu	Gly	Asn	Gln	Tyr	Val	Asn	Val	Met	Asn	Met	Leu	
			455					460					465				
	CTT	TTC	ACA	CTC	CCT	GGA	ACT	CCT	ATA	ACT	TAC	TAT	GGA	GAA	GAA	ATT	1496
25	Leu	Phe	Thr	Leu	Pro	Gly	Thr	Pro	Ile	Thr	Tyr	Tyr	Gly	Glu	Glu	Ile	
		470					475					480					
	GGA	ATG	GGA	AAT	ATT	GTA	GCC	GCA	AAT	CTC	AAT	GAA	AGC	TAT	GAT	ATT	1544
	Gly	Met	Gly	Asn	Ile	Val	Ala	Ala	Asn	Leu	Asn	Glu	Ser	Tyr	Asp	Ile	
		485				490					495					500	
	AAT	ACC	CTT	CGC	TCA	AAG	TCA	CCA	ATG	CAG	TGG	GAC	AAT	AGT	TCA	AAT	1592
	Asn	Thr	Leu	Arg	Ser	Lys	Ser	Pro	Met	Gln	Trp	Asp	Asn	Ser	Ser	Asn	
				505						510					515		
30	GCT	GGT	TTT	TCT	GAA	GCT	AGT	AAC	ACC	TGG	TTA	CCT	ACC	AAT	TCA	GAT	1640
	Ala	Gly	Phe	Ser	Glu	Ala	Ser	Asn	Thr	Trp	Leu	Pro	Thr	Asn	Ser	Asp	

		520		525		530													
		TAC	CAC	ACT	GTG	AAT	GTT	GAT	GTC	CAA	AAG	ACT	CAG	CCC	AGA	TCG	GCT	1688	
		Tyr	His	Thr	Val	Asn	Val	Asp	Val	Gln	Lys	Thr	Gln	Pro	Arg	Ser	Ala		
				535					540					545					
		TTG	AAG	TTA	TAT	CAA	GAT	TTA	AGT	CTA	CTT	CAT	GCC	AAT	GAG	CTA	CTC	1736	
5		Leu	Lys	Leu	Tyr	Gln	Asp	Leu	Ser	Leu	Leu	His	Ala	Asn	Glu	Leu	Leu		
			550					555					560						
		CTC	AAC	AGG	GGC	TGG	TTT	TGC	CAT	TTG	AGG	AAT	GAC	AGC	CAC	TAT	GTT	1784	
		Leu	Asn	Arg	Gly	Trp	Phe	Cys	His	Leu	Arg	Asn	Asp	Ser	His	Tyr	Val		
							570					575					580		
		GTG	TAC	ACA	AGA	GAG	CTG	GAT	GGC	ATC	GAC	AGA	ATC	TTT	ATC	GTG	GTT	1832	
		Val	Tyr	Thr	Arg	Glu	Leu	Asp	Gly	Ile	Asp	Arg	Ile	Phe	Ile	Val	Val		
						585					590					595			
10		CTG	AAT	TTT	GGA	GAA	TCA	ACA	CTG	TTA	AAT	CTA	CAT	AAT	ATG	ATT	TCG	1880	
		Leu	Asn	Phe	Gly	Glu	Ser	Thr	Leu	Leu	Asn	Leu	His	Asn	Met	Ile	Ser		
					600					605					610				
		GGC	CTT	CCC	GCT	AAA	ATA	AGA	ATA	AGG	TTA	AGT	ACC	AAT	TCT	GCC	GAC	1928	
		Gly	Leu	Pro	Ala	Lys	Ile	Arg	Ile	Arg	Leu	Ser	Thr	Asn	Ser	Ala	Asp		
				615					620					625					
		AAA	GGC	AGT	AAA	GTT	GAT	ACA	AGT	GGC	ATT	TTT	CTG	GAC	AAG	GGA	GAG	1976	
15		Lys	Gly	Ser	Lys	Val	Asp	Thr	Ser	Gly	Ile	Phe		Leu	Asp	Lys	Gly		
			630					635					640						
		GGA	CTC	ATC	TTT	GAA	CAC	AAC	ACG	AAG	AAT	CTC	CTT	CAT	CGC	CAA	ACA	2024	
		Gly	Leu	Ile	Phe	Glu	His	Asn	Thr	Lys	Asn	Leu	Leu	His	Arg	Gln	Thr		
			645				650				655						660		
		GCT	TTC	AGA	GAT	AGA	TGC	TTT	GTT	TCC	AAT	CGA	GCA	TGC	TAT	TCC	AGT	2072	
		Ala	Phe	Arg	Asp	Arg	Cys	Phe	Val	Ser	Asn	Arg	Ala	Cys	Tyr	Ser	Ser		
						665					670					675			
20		GTA	CTG	AAC	ATA	CTG	TAT	ACC	TCG	TGT	TAGGCACCTT	TATGAAGAGA	TGAAGAC	2126					
		Val	Leu	Asn	Ile	Leu	Tyr	Thr	Ser	Cys									
					680					685									
		ACTGGCATT	TTT	CAGTGGGATT	GTAAGCATT	TTT	GTAATAGCTT	CATGTACAGC	ATGCTGCTTG	2186									
		GTGAACAATC	ATTAATTCTT	CGATATTTCT	GTAAGCATT	TTT	GTAATAGCTT	CATGTACAGC	ATGCTGCTTG	2246									
		TTCTCAAATG	TTTTGAAAAA	AATAAAATGT	TTAAAGT					2284									

(2) INFORMATION FOR SEQ ID NO:181:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 685 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

30 Met Ala Glu Asp Lys Ser Lys Arg Asp Ser Ile Glu Met Ser Met Lys  
 1 5 10 15  
 Gly Cys Gln Thr Asn Asn Gly Phe Val His Asn Glu Asp Ile Leu Glu



				20				25				30				
	Gln	Thr	Pro	Asp	Pro	Gly	Ser	Ser	Thr	Asp	Asn	Leu	Lys	His	Ser	Thr
			35					40					45			
	Arg	Gly	Ile	Leu	Gly	Ser	Gln	Glu	Pro	Asp	Phe	Lys	Gly	Val	Gln	Pro
		50					55					60				
	Tyr	Ala	Gly	Met	Pro	Lys	Glu	Val	Leu	Phe	Gln	Phe	Ser	Gly	Gln	Ala
	65					70					75				80	
5	Arg	Tyr	Arg	Ile	Pro	Arg	Glu	Ile	Leu	Phe	Trp	Leu	Thr	Val	Ala	Ser
					85					90				95		
	Val	Leu	Val	Leu	Ile	Ala	Ala	Thr	Ile	Ala	Ile	Ile	Ala	Leu	Ser	Pro
				100					105					110		
	Lys	Cys	Leu	Asp	Trp	Trp	Gln	Glu	Gly	Pro	Met	Tyr	Gln	Ile	Tyr	Pro
		115					120						125			
	Arg	Ser	Phe	Lys	Asp	Ser	Asn	Lys	Asp	Gly	Asn	Gly	Asp	Leu	Lys	Gly
	130						135					140				
	Ile	Gln	Asp	Lys	Leu	Asp	Tyr	Ile	Thr	Ala	Leu	Asn	Ile	Lys	Thr	Val
	145					150					155				160	
10	Trp	Ile	Thr	Ser	Phe	Tyr	Lys	Ser	Ser	Leu	Lys	Asp	Phe	Arg	Tyr	Gly
					165					170				175		
	Val	Glu	Asp	Phe	Arg	Glu	Val	Asp	Pro	Ile	Phe	Gly	Thr	Met	Glu	Asp
				180					185					190		
	Phe	Glu	Asn	Leu	Val	Ala	Ala	Ile	His	Asp	Lys	Gly	Leu	Lys	Leu	Ile
		195						200					205			
	Ile	Asp	Phe	Ile	Pro	Asn	His	Thr	Ser	Asp	Lys	His	Ile	Trp	Phe	Gln
	210					215						220				
	Leu	Ser	Arg	Thr	Arg	Thr	Gly	Lys	Tyr	Thr	Asp	Tyr	Tyr	Ile	Trp	His
	225					230					235				240	
15	Asp	Cys	Thr	His	Glu	Asn	Gly	Lys	Thr	Ile	Pro	Pro	Asn	Asn	Trp	Leu
				245						250				255		
	Ser	Val	Tyr	Gly	Asn	Ser	Ser	Trp	His	Phe	Asp	Glu	Val	Arg	Asn	Gln
				260				265						270		
	Cys	Tyr	Phe	His	Gln	Phe	Met	Lys	Glu	Gln	Pro	Asp	Leu	Asn	Phe	Arg
		275						280					285			
	Asn	Pro	Asp	Val	Gln	Glu	Glu	Ile	Lys	Glu	Ile	Leu	Arg	Phe	Trp	Leu
		290				295						300				
	Thr	Lys	Gly	Val	Asp	Gly	Phe	Ser	Leu	Asp	Ala	Val	Lys	Phe	Leu	Leu
	305					310					315				320	
20	Glu	Ala	Lys	His	Leu	Arg	Asp	Glu	Ile	Gln	Val	Asn	Lys	Thr	Gln	Ile
				325						330					335	
	Pro	Asp	Thr	Val	Thr	Gln	Tyr	Ser	Glu	Leu	Tyr	His	Asp	Phe	Thr	Thr
				340					345					350		
	Thr	Gln	Val	Gly	Met	His	Asp	Ile	Val	Arg	Ser	Phe	Arg	Gln	Thr	Met
		355					360						365			
	Asp	Gln	Tyr	Ser	Thr	Glu	Pro	Gly	Arg	Tyr	Arg	Phe	Met	Gly	Thr	Glu
	370					375						380				
	Ala	Tyr	Ala	Glu	Ser	Ile	Asp	Arg	Thr	Val	Met	Tyr	Tyr	Gly	Leu	Pro
	385					390					395				400	
	Phe	Ile	Gln	Glu	Ala	Asp	Phe	Pro	Phe	Asn	Asn	Tyr	Leu	Ser	Met	Leu
				405						410					415	
25	Asp	Thr	Val	Ser	Gly	Asn	Ser	Val	Tyr	Glu	Val	Ile	Thr	Ser	Trp	Met
				420					425					430		
	Glu	Asn	Met	Pro	Glu	Gly	Lys	Trp	Pro	Asn	Trp	Met	Ile	Gly	Gly	Pro
		435					440						445			
	Asp	Ser	Ser	Arg	Leu	Thr	Ser	Arg	Leu	Gly	Asn	Gln	Tyr	Val	Asn	Val
	450					455						460				
	Met	Asn	Met	Leu	Leu	Phe	Thr	Leu	Pro	Gly	Thr	Pro	Ile	Thr	Tyr	Tyr
	465					470					475				480	
	Gly	Glu	Glu	Ile	Gly	Met	Gly	Asn	Ile	Val	Ala	Ala	Asn	Leu	Asn	Glu
				485						490					495	
30	Ser	Tyr	Asp	Ile	Asn	Thr	Leu	Arg	Ser	Lys	Ser	Pro	Met	Gln	Trp	Asp
				500					505					510		

Asn Ser Ser Asn Ala Gly Phe Ser Glu Ala Ser Asn Thr Trp Leu Pro  
           515                          520                          525  
 Thr Asn Ser Asp Tyr His Thr Val Asn Val Asp Val Gln Lys Thr Gln  
       530                          535                          540  
 Pro Arg Ser Ala Leu Lys Leu Tyr Gln Asp Leu Ser Leu Leu His Ala  
 545                          550                          555                          560  
 Asn Glu Leu Leu Leu Asn Arg Gly Trp Phe Cys His Leu Arg Asn Asp  
                           565                          570                          575  
**5** Ser His Tyr Val Val Tyr Thr Arg Glu Leu Asp Gly Ile Asp Arg Ile  
                           580                          585                          590  
 Phe Ile Val Val Leu Asn Phe Gly Glu Ser Thr Leu Leu Asn Leu His  
                           595                          600                          605  
 Asn Met Ile Ser Gly Leu Pro Ala Lys Ile Arg Ile Arg Leu Ser Thr  
       610                          615                          620  
 Asn Ser Ala Asp Lys Gly Ser Lys Val Asp Thr Ser Gly Ile Phe Leu  
 625                          630                          635                          640  
 Asp Lys Gly Glu Gly Leu Ile Phe Glu His Asn Thr Lys Asn Leu Leu  
                           645                          650                          655  
**10** His Arg Gln Thr Ala Phe Arg Asp Arg Cys Phe Val Ser Asn Arg Ala  
                           660                          665                          670  
 Cys Tyr Ser Ser Val Leu Asn Ile Leu Tyr Thr Ser Cys  
                           675                          680                          685

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 54 amino acids  
       (B) TYPE: amino acid  
**15**      (C) STRANDEDNESS:  
       (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Leu Val Pro Arg Gly Ser Pro Gly Ile Pro Gly Ser Arg Val Gly Gln  
   1                          5                          10                          15  
 Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala Arg Ser Cys Ala His  
                           20                          25                          30  
**20** Gln Gly Cys Gly Ala Gly Thr Arg Asn Ser His Gly Cys Ile Thr Arg  
                           35                          40                          45  
 Pro Leu Arg Gln Ala Ser  
       50

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 19 amino acids  
**25**      (B) TYPE: amino acid  
       (C) STRANDEDNESS:  
       (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Ser Ala Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val Arg  
   1                          5                          10                          15  
**30** Leu Asn Gly

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Asp Gly Ser Arg Ala Val Arg Leu Asn Gly Val Glu Asn Ala Asn Thr  
 1 5 10 15  
 Arg Lys Ser Ser Arg  
 20

(2) INFORMATION FOR SEQ ID NO:185:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

15 Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg  
 1 5 10 15  
 Arg His Pro

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly  
 1 5 10

25 (2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Ser Arg Pro Tyr Ser Val Asp Ser Asp Ser Asp Thr Asn Ala Lys His  
 1 5 10 15  
 Ser Ser His Asn Arg  
 20

(2) INFORMATION FOR SEQ ID NO:188:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

10 Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg Ser  
 1 5 10 15  
 Arg Pro Asn

(2) INFORMATION FOR SEQ ID NO:189:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Arg Tyr Lys His Asp Ile Gly Cys Asp Ala Gly Val Asp Lys Lys Ser  
 1 5 10 15  
 Ser Ser Val Arg Gly Gly Cys Gly  
 20

20 (2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Gly Cys Asp Ala Gly Val Asp Lys Lys Ser Ser Ser Val Arg Gly Gly  
 1 5 10 15  
 Cys Gly Ala His Ser Ser Pro Pro Arg Ala  
 20 25

(2) INFORMATION FOR SEQ ID NO:191:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 amino acids  
 (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

5 Gly Ala His Ser Ser Pro Pro Arg Ala Gly Arg Gly Pro Arg Gly Thr  
1 5 10 15  
Met Val Ser Arg Leu  
20

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:193:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

20 Lys Lys Arg Ile Ala Gly Leu Pro Trp Tyr Arg Cys Arg Thr Val Ala  
1 5 10 15  
Phe Glu Thr Gly Met Gln Asn Thr Gln Leu Cys Ser Thr Ile Val Gln  
20 25 30  
Leu Ser Phe Thr Pro Glu Glu  
35

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

25

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

30 Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 9 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Ser Asn Pro Arg Gly Arg Arg His Pro  
 1 5

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 9 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

10 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Thr Asn Ala Lys His Ser Ser His Asn  
 1 5

15 (2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 10 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Ser Ser His Asn Arg Arg Leu Arg Thr Arg  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 10 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

25 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn  
 1 5 10

30 (2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Arg Val Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala Arg  
 1 5 10 15  
 Ser Cys Ala

(2) INFORMATION FOR SEQ ID NO:200:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

15 Val Arg Arg Pro Trp Ala Arg Ser Cys Ala His Gln Gly Cys Gly Ala  
 1 5 10 15  
 Gly Thr Arg Asn Ser  
 20

(2) INFORMATION FOR SEQ ID NO:201:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

Gly Thr Arg Asn Ser His Gly Cys Ile Thr Arg Pro Leu Arg Gln Ala  
 1 5 10 15  
 Ser Gln His

25 (2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 40 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp  
 1 5 10 15  
 Ser Asp Ser Asp Thr Met Ala Lys His Ser Ser His Asn Arg Arg Leu  
 20 25 30  
 Arg Thr Arg Ser Arg Pro Asn Gly  
 35 40

(2) INFORMATION FOR SEQ ID NO:203:

5

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

10

Tyr Ser Lys Val  
 1

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

15

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Phe Pro His Leu  
 1

(2) INFORMATION FOR SEQ ID NO:205:

20

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

25

Tyr Arg Gly Val  
 1

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

30

(ii) MOLECULE TYPE: peptide



(

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Tyr Gln Thr Ile  
1

(2) INFORMATION FOR SEQ ID NO:207:

5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 4 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

10 Thr Glu Gln Phe  
1

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 4 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

15 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Thr Glu Val Met  
1

(2) INFORMATION FOR SEQ ID NO:209:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 4 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

25 Thr Ser Ala Phe  
1

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 4 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

30 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Tyr Thr Arg Phe  
1

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 717 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...714

(D) OTHER INFORMATION:

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

	ATG TCC CCT ATA CTA GGT TAT TGG AAA ATT AAG GGC CTT GTG CAA CCC	48
	Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro	
	1 5 10 15	
	ACT CGA CTT CTT TTG GAA TAT CTT GAA GAA AAA TAT GAA GAG CAT TTG	96
	Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
	20 25 30	
15	TAT GAG CGC GAT GAA GGT GAT AAA TGG CGA AAC AAA AAG TTT GAA TTG	144
	Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
	35 40 45	
	GGT TTG GAG TTT CCC AAT CTT CCT TAT TAT ATT GAT GGT GAT GTT AAA	192
	Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
	50 55 60	
	TTA ACA CAG TCT ATG GCC ATC ATA CGT TAT ATA GCT GAC AAG CAC AAC	240
20	Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
	65 70 75 80	
	ATG TTG GGT GGT TGT CCA AAA GAG CGT GCA GAG ATT TCA ATG CTT GAA	288
	Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
	85 90 95	
	GGA GCG GTT TTG GAT ATT AGA TAC GGT GTT TCG AGA ATT GCA TAT AGT	336
	Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
	100 105 110	
25	AAA GAC TTT GAA ACT CTC AAA GTT GAT TTT CTT AGC AAG CTA CCT GAA	384
	Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
	115 120 125	
	ATG CTG AAA ATG TTC GAA GAT CGT TTA TGT CAT AAA ACA TAT TTA AAT	432
	Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
	130 135 140	
	GGT GAT CAT GTA ACC CAT CCT GAC TTC ATG TTG TAT GAC GCT CTT GAT	480
30	Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
	145 150 155 160	

	GTT GTT TTA TAC ATG GAC CCA ATG TGC CTG GAT GCG TTC CCA AAA TTA	528
	Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
	165 170 175	
	GTT TGT TTT AAA AAA CGT ATT GAA GCT ATC CCA CAA ATT GAT AAG TAC	576
	Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
	180 185 190	
5	TTG AAA TCC AGC AAG TAT ATA GCA TGG CCT TTG CAG GGC TGG CAA GCC	624
	Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
	195 200 205	
	ACG TTT GGT GGT GGC GAC CAT CCT CCA AAA TCG GAT CTG GTT CCG CGT	672
	Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
	210 215 220	
	GGA TCC CCA GGA ATT CCC GGG TCG ACT CGA GCG GCC GCA TCG TGA	717
	Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser	
10	225 230 235	

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

15

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

	Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro	
	1 5 10 15	
	Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
	20 25 30	
	Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
	35 40 45	
20	Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
	50 55 60	
	Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
	65 70 75 80	
	Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
	85 90 95	
	Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
	100 105 110	
	Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
	115 120 125	
25	Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
	130 135 140	
	Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
	145 150 155 160	
	Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
	165 170 175	
	Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
	180 185 190	
	Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
	195 200 205	
30	Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
	210 215 220	

Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser  
 225 230 235

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

5

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

	Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro
	1				5				10						15	
	Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu
10				20					25					30		
	Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu
			35					40					45			
	Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys
		50					55					60				
	Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn
	65					70					75					80
	Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu
				85						90					95	
	Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser
				100					105					110		
15	Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu
			115						120					125		
	Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn
		130					135					140				
	Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp
	145					150					155					160
	Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu
				165						170					175	
	Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr
				180					185					190		
20	Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala
			195					200					205			
	Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg
		210				215						220				
	Gly	Ser	Pro	Gly	Ile	Pro	Gly	Ser	Thr	Arg	Ala	Ala	Ala	Ser	Ser	Gln
	225					230					235					240
	Gly	Ser	Lys	Gln	Cys	Met	Gln	Tyr	Arg	Thr	Gly	Arg	Leu	Thr	Val	Gly
				245						250					255	
	Ser	Glu	Tyr	Gly	Cys	Gly	Met	Asn	Pro	Ala	Arg	His	Ala	Thr	Pro	Ala
				260					265					270		
25	Tyr	Pro	Ala	Arg	Leu	Leu	Pro	Arg	Tyr	Arg						
			275					280								

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

30

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

```

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1      5      10      15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
      20      25      30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
      35      40      45
5 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50      55      60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65      70      75      80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
      85      90      95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100      105      110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115      120      125
10 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130      135      140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145      150      155      160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
      165      170      175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180      185      190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195      200      205
15 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210      215      220
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Asp
225      230      235      240
His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys Glu Pro Gly
      245      250      255
Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg Lys Val Phe
260      265      270
Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr
275      280

```

20

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

```

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1      5      10      15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
      20      25      30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
      35      40      45
30 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50      55      60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65      70      75      80

```

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 5 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 10 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Pro  
 225 230 235 240  
 Cys Gly Gly Ser Trp Gly Arg Phe Met Gln Gly Gly Leu Phe Gly Gly  
 245 250 255  
 Arg Thr Asp Gly Cys Gly Ala His Arg Asn Arg Thr Ser Ala Ser Leu  
 260 265 270  
 Glu Pro Pro Ser Ser Asp Tyr  
 275

(2) INFORMATION FOR SEQ ID NO:216:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

20 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15  
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 25 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 30 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
180 185 190  
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
195 200 205  
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
210 215 220  
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Arg Gly  
225 230 235 240  
5 Ser Thr Gly Thr Ala Gly Gly Glu Arg Ser Gly Val Leu Asn Leu His  
245 250 255  
Thr Arg Asp Asn Ala Ser Gly Ser Gly Phe Lys Pro Trp Tyr Pro Ser  
260 265 270  
Asn Arg Gly His Lys  
275

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 277 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
1 5 10 15  
15 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
20 25 30  
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
35 40 45  
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
50 55 60  
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
65 70 75 80  
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
85 90 95  
20 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
100 105 110  
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
115 120 125  
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
130 135 140  
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
145 150 155 160  
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
165 170 175  
25 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
180 185 190  
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
195 200 205  
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
210 215 220  
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser His  
225 230 235 240  
Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe Arg Glu Leu Arg  
245 250 255  
30 Asp Arg Trp Asn Ala Thr Ser His His Thr Arg Pro Thr Pro Gln Leu  
260 265 270

Pro Arg Gly Pro Asn  
275

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
1 5 10 15  
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
20 25 30  
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
35 40 45  
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
50 55 60  
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
65 70 75 80  
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
85 90 95  
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
100 105 110  
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
115 120 125  
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
130 135 140  
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
145 150 155 160  
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
165 170 175  
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
180 185 190  
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
195 200 205  
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
210 215 220  
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser His  
225 230 235 240  
Ser Gly Gly Met Asn Arg Ala Tyr  
245

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro



	1		5		10		15
	Thr	Arg	Leu	Leu	Glu	Tyr	Leu
			20				25
	Tyr	Glu	Arg	Asp	Glu	Gly	Asp
			35				40
	Gly	Leu	Glu	Phe	Pro	Asn	Leu
			50				55
	Leu	Thr	Gln	Ser	Met	Ala	Ile
5	65				70		Ile
	Met	Leu	Gly	Gly	Cys	Pro	Lys
				85			90
	Gly	Ala	Val	Leu	Asp	Ile	Arg
			100				105
	Lys	Asp	Phe	Glu	Thr	Leu	Lys
			115				120
	Met	Leu	Lys	Met	Phe	Glu	Asp
			130				135
	Gly	Asp	His	Val	Thr	His	Pro
10	145						150
	Val	Val	Leu	Tyr	Met	Asp	Pro
					165		170
	Val	Cys	Phe	Lys	Lys	Arg	Ile
			180				185
	Leu	Lys	Ser	Ser	Lys	Tyr	Ile
			195				200
	Thr	Phe	Gly	Gly	Gly	Asp	His
			210				215
	Gly	Ser	Pro	Gly	Ile	Pro	Gly
15	225					230	
	Val	Phe	Arg	Glu	Leu	Arg	Asp
							245

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

20

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

	Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro
	1				5				10						15	
	Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu
			20						25					30		
25	Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu
			35					40					45			
	Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys
			50				55					60				
	Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn
	65					70					75				80	
	Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu
				85						90					95	
	Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser
			100						105					110		
30	Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu
			115					120					125			
	Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn

	130		135		140
	Gly Asp His Val Thr His	Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp			
	145	150	155	160	
	Val Val Leu Tyr Met Asp	Pro Met Cys Leu Asp Ala Phe Pro Lys Leu			
		165	170	175	
	Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr				
		180	185	190	
	Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala				
5		195	200	205	
	Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg				
		210	215	220	
	Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Trp Asn				
		225	230	235	240
	Ala Thr Ser His His Thr Arg Pro				
		245			

(2) INFORMATION FOR SEQ ID NO:221:

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 247 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

15	Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro	
	1	5 10 15
	Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
		20 25 30
	Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
		35 40 45
	Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
		50 55 60
	Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
		65 70 75 80
20	Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
		85 90 95
	Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
		100 105 110
	Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
		115 120 125
	Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
		130 135 140
	Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
		145 150 155 160
25	Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
		165 170 175
	Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
		180 185 190
	Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
		195 200 205
	Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
		210 215 220
	Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Thr Pro	
		225 230 235 240
30	Gln Leu Pro Arg Gly Pro Asn	
		245

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

```
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1      5      10      15
Thr Arg Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu
 20      25      30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35      40      45
10 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50      55      60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65      70      75      80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85      90      95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100      105      110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115      120      125
15 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130      135      140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145      150      155      160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165      170      175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180      185      190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195      200      205
20 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210      215      220
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Gly Asp
225      230      235      240
Val Phe Arg Glu Leu Arg Asp Arg Trp Asn Ala Thr Ser His His Thr
245      250      255
Arg Pro
```

(2) INFORMATION FOR SEQ ID NO:223:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

```
30 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1      5      10      15
```

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 5 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 10 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ser Trp Asn  
 225 230 235 240  
 15 Ala Thr Ser His His Thr Arg Pro Thr Pro Gln Leu Pro Arg Gly Pro  
 245 250 255  
 Asn

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 267 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown  
 20

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15  
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
 25 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 30 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125

	Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn
	130						135					140				
	Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp
	145					150					155					160
	Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu
					165					170					175	
	Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr
				180					185					190		
5	Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala
		195						200					205			
	Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg
	210					215						220				
	Gly	Ser	Pro	Gly	Ile	Pro	Gly	Ser	Thr	Arg	Ala	Ala	Ala	Ser	Gly	Asp
	225					230					235					240
	Val	Phe	Arg	Glu	Leu	Arg	Asp	Arg	Trp	Asn	Ala	Thr	Ser	His	His	Thr
				245						250					255	
	Arg	Pro	Thr	Pro	Gln	Leu	Pro	Arg	Gly	Pro	Asn					
				260					265							

10

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 277 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

	Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro
	1				5					10					15	
	Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Lys	Tyr	Glu	Glu	His	Leu	
			20						25				30			
	Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu
			35					40				45				
	Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys
	50					55					60					
20	Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn
	65					70				75					80	
	Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu
					85					90					95	
	Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser
				100					105					110		
	Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu
			115					120					125			
	Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn
	130						135					140				
25	Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp
	145					150					155					160
	Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu
					165					170					175	
	Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr
				180					185					190		
	Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala
		195						200					205			
	Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg
	210					215						220				
30	Gly	Ser	Pro	Gly	Ile	Pro	Gly	Ser	Thr	Arg	Ala	Ala	Ala	Ser	Ser	His
	225					230					235					240

Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe Arg Glu Leu Arg  
245 250 255  
Asp Arg Trp Asn Ala Thr Ser Ala Ala Thr Arg Pro Thr Pro Gln Leu  
260 265 270  
Pro Arg Gly Pro Asn  
275

(2) INFORMATION FOR SEQ ID NO:226:

5

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 277 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

10

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
1 5 10 15  
Thr Arg Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu  
20 25 30  
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
35 40 45  
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
50 55 60  
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
65 70 75 80  
15 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
85 90 95  
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
100 105 110  
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
115 120 125  
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
130 135 140  
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
145 150 155 160  
20 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
165 170 175  
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
180 185 190  
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
195 200 205  
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
210 215 220  
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Ala  
225 230 235 240  
25 Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val Arg Leu Asn  
245 250 255  
Gly Val Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg  
260 265 270  
Gly Arg Arg His Pro  
275

(2) INFORMATION FOR SEQ ID NO:227:

30

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 257 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

```

5 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
  1      5      10      15
  Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
    20      25      30
  Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
    35      40      45
  Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
    50      55      60
  Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
    65      70      75      80
10 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
    85      90      95
  Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
    100      105      110
  Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
    115      120      125
  Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
    130      135      140
  Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
    145      150      155      160
15 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
    165      170      175
  Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
    180      185      190
  Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
    195      200      205
  Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
    210      215      220
  Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Ala
    225      230      235      240
20 Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val Arg Leu Asn
    245      250      255
  Gly

```

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

```

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1      5      10      15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu
  20      25      30
30 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
    35      40      45

```

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 5 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 10 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Asp Gly  
 225 230 235 240  
 Ser Arg Ala Val Arg Leu Asn Gly Val Glu Asn Ala Asn Thr Arg Lys  
 245 250 255  
 Ser Ser Arg

15 (2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 257 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15  
 Thr Arg Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 25 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 30 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160



Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 5 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Glu Asn  
 225 230 235 240  
 Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg Arg His  
 245 250 255  
 Pro

(2) INFORMATION FOR SEQ ID NO:230:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 248 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

15 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15  
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 20 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 25 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Glu Asn  
 225 230 235 240  
 Ala Asn Thr Arg Lys Ser Ser Arg  
 245

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 248 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

	Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro
	1				5				10						15	
	Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu
			20						25					30		
	Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu
		35						40					45			
	Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys
	50					55						60				
10	Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn
	65				70					75					80	
	Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu
				85					90						95	
	Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser
			100						105					110		
	Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu
		115						120					125			
	Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn
	130					135						140				
15	Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp
	145					150					155					160
	Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu
				165					170						175	
	Val	Cys	Phe	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	
		180						185					190			
	Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala
		195						200					205			
	Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg
	210					215						220				
20	Gly	Ser	Pro	Gly	Ile	Pro	Gly	Ser	Thr	Arg	Ala	Ala	Ala	Ser	Arg	Lys
	225				230					235						240
	Ser	Ser	Arg	Ser	Asn	Pro	Arg	Gly								
					245											

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 247 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

25

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

	Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro
	1				5				10						15	
	Thr	Arg	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu	
			20					25					30			
30	Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu
		35						40					45			

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 5 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 10 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Asn  
 225 230 235 240  
 Pro Arg Gly Arg Arg His Pro  
 245

(2) INFORMATION FOR SEQ ID NO:233:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

20 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15  
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 25 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 30 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
180 185 190  
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
195 200 205  
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
210 215 220  
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ser Thr Arg  
225 230 235 240  
5 Lys Ser Ser Arg Ser Asn Pro Arg Gly  
245

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
1 5 10 15  
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
20 25 30  
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
35 40 45  
15 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
50 55 60  
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
65 70 75 80  
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
85 90 95  
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
100 105 110  
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
115 120 125  
20 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
130 135 140  
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
145 150 155 160  
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
165 170 175  
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
180 185 190  
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
195 200 205  
25 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
210 215 220  
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ser Ser Thr  
225 230 235 240  
Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp Ser Asp  
245 250 255  
Ser Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr  
260 265 270  
Arg Ser Arg Pro Asn  
275  
30

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

	Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro	
	1				5				10						15		
	Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu	
			20						25					30			
	Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu	
			35					40					45				
	Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys	
		50				55						60					
10	Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn	
	65				70					75					80		
	Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu	
				85					90						95		
	Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	
			100						105					110			
	Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	
		115						120					125				
	Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	
		130				135						140					
15	Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	
	145				150						155					160	
	Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	
				165					170						175		
	Val	Cys	Phe	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr		
			180					185					190				
	Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	
		195						200					205				
	Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	
		210				215						220					
20	Gly	Ser	Pro	Gly	Ile	Pro	Gly	Ser	Thr	Arg	Ala	Ala	Ala	Ser	Ser	Thr	
	225				230						235					240	
	Pro	Pro	Ser	Arg	Glu	Ala	Tyr	Ser	Arg	Pro	Tyr	Ser	Val	Asp	Ser	Asp	
				245						250					255		
	Ser	Asp															

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- 25
- (A) LENGTH: 259 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

	Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro	
	1				5				10						15		
30	Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu	
			20						25					30			

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 5 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 10 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Arg  
 225 230 235 240  
 Pro Tyr Ser Val Asp Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser  
 245 250 255  
 15 His Asn Arg

(2) INFORMATION FOR SEQ ID NO:237:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 257 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15  
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 25 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 30 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140

	Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp
	145					150					155					160
	Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu
					165					170					175	
	Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr
				180					185					190		
	Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala
			195					200					205			
5	Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg
	210					215						220				
	Gly	Ser	Pro	Gly	Ile	Pro	Gly	Ser	Thr	Arg	Ala	Ala	Ala	Ser	Thr	Asn
	225					230					235					240
	Ala	Lys	His	Ser	Ser	His	Asn	Arg	Arg	Leu	Arg	Thr	Arg	Ser	Arg	Pro
					245					250						255
	Asn															

(2) INFORMATION FOR SEQ ID NO:238:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

15

	Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro
	1				5				10						15	
	Thr	Arg	Leu	Leu	Glu	Tyr	Leu	Glu	Lys	Tyr	Glu	Glu	His	Leu		
				20				25					30			
	Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu
			35				40					45				
	Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys
		50				55					60					
	Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn
	65				70					75						80
20	Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu
				85				90						95		
	Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser
			100					105					110			
	Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu
			115				120						125			
	Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn
		130					135					140				
	Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp
	145					150					155					160
25	Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu
					165					170					175	
	Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr
				180					185					190		
	Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala
			195					200					205			
	Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg
		210				215						220				
	Gly	Ser	Pro	Gly	Ile	Pro	Gly	Ser	Thr	Arg	Ala	Ala	Ala	Ser	Thr	Asn
	225					230					235					240
30	Ala	Lys	His	Ser	Ser	His	Asn									
					245											

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

```
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1      5      10      15
Thr Arg Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu
 20      25      30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35      40      45
10 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50      55      60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65      70      75      80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85      90      95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100      105      110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115      120      125
15 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130      135      140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145      150      155      160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165      170      175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180      185      190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195      200      205
20 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210      215      220
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Ser
225      230      235      240
His Asn Arg Arg Leu Arg Thr Arg
245
```

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 248 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

```
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1      5      10      15
30 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20      25      30
```



Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 5 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 10 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Arg Arg  
 225 230 235 240  
 Leu Arg Thr Arg Ser Arg Pro Asn  
 245

15

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15  
 Thr Arg Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 25 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 30 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 5 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ser Arg Val  
 225 230 235 240  
 Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala Arg Ser Cys  
 245 250 255  
 Ala His Gln Gly Cys Gly Ala Gly Thr Arg Asn Ser His Gly Cys Ile  
 260 265 270  
 Thr Arg Pro Leu Arg Gln Ala Ser Ala His  
 275 280

(2) INFORMATION FOR SEQ ID NO:242:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

15

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15  
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 20 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 25 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ser Arg Val  
 225 230 235 240  
 30 Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala Arg Ser Cys  
 245 250 255

Ala

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
1 5 10 15  
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
20 25 30  
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
35 40 45  
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
50 55 60  
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
65 70 75 80  
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
85 90 95  
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
100 105 110  
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
115 120 125  
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
130 135 140  
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
145 150 155 160  
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
165 170 175  
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
180 185 190  
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
195 200 205  
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
210 215 220  
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Val Arg  
225 230 235 240  
Arg Pro Trp Ala Arg Ser Cys Ala His Gln Gly Cys Gly Ala Gly Thr  
245 250 255  
Arg Asn Ser

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

	Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro
	1				5					10					15	
	Thr	Arg	Leu	Leu	Glu	Tyr	Leu	Glu	Lys	Tyr	Glu	Glu	His	Leu		
			20					25					30			
	Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu
		35					40					45				
	Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys
		50				55					60					
5	Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn
	65				70					75					80	
	Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu
				85					90						95	
	Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser
			100						105					110		
	Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu
		115					120						125			
	Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn
		130					135					140				
10	Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp
		145				150					155				160	
	Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu
				165					170						175	
	Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr
			180						185					190		
	Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala
		195						200					205			
	Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg
		210				215						220				
15	Gly	Ser	Pro	Gly	Ile	Pro	Gly	Ser	Thr	Arg	Ala	Ala	Ala	Ser	Gly	Thr
		225				230					235				240	
	Arg	Asn	Ser	His	Gly	Cys	Ile	Thr	Arg	Pro	Leu	Arg	Gln	Ala	Ser	Gln
					245					250					255	
	His															

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 282 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

	Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro
	1				5					10					15	
25	Thr	Arg	Leu	Leu	Glu	Tyr	Leu	Glu	Lys	Tyr	Glu	Glu	His	Leu		
			20					25					30			
	Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu
		35					40					45				
	Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys
		50				55					60					
	Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn
		65			70					75					80	
	Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu
				85					90						95	
30	Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser
			100						105					110		

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 5 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ser Arg Tyr  
 225 230 235 240  
 Lys His Asp Ile Gly Cys Asp Ala Gly Val Asp Lys Lys Ser Ser Ser  
 245 250 255  
 10 Val Arg Gly Gly Cys Gly Ala His Ser Ser Pro Pro Arg Ala Gly Arg  
 260 265 270  
 Gly Pro Arg Gly Thr Met Val Ser Arg Leu  
 275 280

(2) INFORMATION FOR SEQ ID NO:246:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 262 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

15

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15  
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 25 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 30 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205

Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ser Arg Tyr  
 225 230 235 240  
 Lys His Asp Ile Gly Cys Asp Ala Gly Val Asp Lys Lys Ser Ser Ser  
 245 250 255  
 Val Arg Gly Gly Cys Gly  
 260

5

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15  
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 15 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 20 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 25 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Gly Cys  
 225 230 235 240  
 Asp Ala Gly Val Asp Lys Lys Ser Ser Ser Val Arg Gly Gly Cys Gly  
 245 250 255  
 Ala His Ser Ser Pro Pro Arg Ala  
 260

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid

30

(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

```

5  Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
   1      5      10      15
   Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
      20      25      30
   Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
      35      40      45
   Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
      50      55      60
   Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
      65      70      75      80
   Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
      85      90      95
10  Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
      100      105      110
   Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
      115      120      125
   Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
      130      135      140
   Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
      145      150      155      160
   Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
      165      170      175
15  Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
      180      185      190
   Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
      195      200      205
   Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
      210      215      220
   Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Gly Ala
      225      230      235      240
   His Ser Ser Pro Pro Arg Ala Gly Arg Gly Pro Arg Gly Thr Met Val
      245      250      255
20  Ser Arg Leu

```

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

25

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

```

30  Ser Gly Ser Pro Pro Cys Cys Cys Ser Trp Gly Arg Phe Met Gln Gly
   1      5      10      15
   Gly Leu Phe Gly Gly Arg Thr Asp Gly Cys Gly Ala His Arg Asn Arg
      20      25      30
   Thr Ser Ala Ser Leu Glu Pro Pro Ser Ser Asp Tyr
      35      40

```

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 40 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

Ser	His	Ser	Gly	Gly	Met	Asn	Arg	Ala	Tyr	Gly	Asp	Val	Phe	Arg	Glu
1				5					10					15	
Leu	Arg	Asp	Arg	Trp	Asn	Ala	Thr	Ser	His	His	Thr	Arg	Pro	Thr	Pro
			20					25					30		
Gln	Leu	Pro	Arg	Gly	Pro	Asn	Ser								
		35					40								

10 (2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

Asp	Thr	Asn	Ala	Lys	His	Ser	Ser	His	Asn	Arg	Arg	Leu	Arg	Thr	Arg
1				5					10					15	
Ser	Arg	Pro	Asn	Gly											
			20												

(2) INFORMATION FOR SEQ ID NO:252:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 23 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

Cys	Gly	Ala	Gly	Thr	Arg	Asn	Ser	His	Gly	Cys	Ile	Thr	Arg	Pro	Leu
1				5					10					15	
Arg	Gln	Ala	Ser	Ala	His	Gly									
			20												

(2) INFORMATION FOR SEQ ID NO:253:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown



(

(ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

(A) NAME/KEY: Modified Site  
 (B) LOCATION: 1  
 (D) OTHER INFORMATION: "Xaa=Ser or Thr"

5 (A) NAME/KEY: Modified Site  
 (B) LOCATION: 3  
 (D) OTHER INFORMATION: "Xaa=Arg or Lys"

(A) NAME/KEY: Modified Site  
 (B) LOCATION: 4  
 (D) OTHER INFORMATION: "Xaa=Lys or Arg"

(A) NAME/KEY: Modified Site  
 (B) LOCATION: 6  
 (D) OTHER INFORMATION: "Xaa=Ser or Leu"

10 (A) NAME/KEY: Modified Site  
 (B) LOCATION: 7  
 (D) OTHER INFORMATION: "Xaa=Arg, Ile, Val or Ser"

(A) NAME/KEY: Modified Site  
 (B) LOCATION: 8  
 (D) OTHER INFORMATION: "Xaa=Ser, Tyr, Phe or His"

15 (A) NAME/KEY: Modified Site  
 (B) LOCATION: 10  
 (D) OTHER INFORMATION: "Xaa=Phe, His or Arg"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

Xaa Thr Xaa Xaa Ser Xaa Xaa Xaa Asn Xaa Arg  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:254:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

25 (A) NAME/KEY: Modified Site  
 (B) LOCATION: 2  
 (D) OTHER INFORMATION: "Xaa=Ser, Ala or Gly"

(A) NAME/KEY: Modified Site  
 (B) LOCATION: 4  
 (D) OTHER INFORMATION: "Xaa=Val or Gln"

(A) NAME/KEY: Modified Site  
 (B) LOCATION: 7  
 (D) OTHER INFORMATION: "Xaa=Pro, Gly or Ser"

30 (A) NAME/KEY: Modified Site  
 (B) LOCATION: 8

(D) OTHER INFORMATION: "Xaa=Trp or Tyr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

Asp Xaa Asp Xaa Arg Arg Xaa Xaa  
1 5

5 (2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

10

- (A) NAME/KEY: Modified Site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: "Xaa=Ala or Phe"
- (A) NAME/KEY: Modified Site
- (B) LOCATION: 8
- (D) OTHER INFORMATION: "Xaa=Arg or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NC:255:

15 Val Arg Ser Gly Cys Gly Xaa Xaa Ser Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

20

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

Asn Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:257:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

30 Ser Thr Lys Arg Ser Leu Ile Tyr Asn His Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 10 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

Ser Thr Gly Arg Lys Val Phe Asn Arg Arg  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:259:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

15 Thr Asn Ala Lys His Ser Ser His Asn Arg Arg  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

Asp Ser Asp Val Arg Arg Pro Trp  
 1 5

(2) INFORMATION FOR SEQ ID NO:261:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

30 Ala Ala Asp Gln Arg Arg Gly Trp  
 1 5

(2) INFORMATION FOR SEQ ID NO:262:

- (
- (
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:  
Asp Gly Arg Gly Gly Arg Ser Tyr  
1 5
- (2) INFORMATION FOR SEQ ID NO:263:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
10 (C) STRANDEDNESS:  
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:  
Arg Val Arg Ser  
1
- 15 (2) INFORMATION FOR SEQ ID NO:264:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:  
Ser Val Arg Ser Gly Cys Gly Phe Arg Gly Ser Ser  
1 5 10
- (2) INFORMATION FOR SEQ ID NO:265:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
25 (C) STRANDEDNESS:  
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:  
Ser Val Arg Gly Gly Cys Gly Ala His Ser Ser  
1 5 10
- 30 (2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

5 (A) NAME/KEY: Other  
 (B) LOCATION: 2...2  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

	Cys	Xaa	Phe	Ile	Thr	Lys	Ala	Leu	Gly	Ile	Ser	Tyr	Gly	Arg	Lys	Lys
	1				5				10					15		
10	Arg	Arg	Gln	Arg	Arg	Arg	Pro	Pro	Gln	Gly	Ser	Gln	Thr	His	Gln	Val
			20						25					30		
	Ser	Leu	Ser	Lys	Gln											
			35													

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 18 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

15 (ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

(A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Ac-Cys

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

	Xaa	Leu	Asn	Gly	Gly	Val	Lys	Met	Tyr	Val	Glu	Ser	Val	Asp	Arg	Tyr
	1				5				10					15		
	Val	Cys														

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

25 (ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

(A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Ac-Cys

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

Xaa Leu Asn Gly Gly Val Lys Phe Ile Thr Cys Met Tyr Val Glu Ser  
1 5 10 15  
Val Asp Arg Tyr Val Cys  
20

(2) INFORMATION FOR SEQ ID NO:269:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

10

- (A) NAME/KEY: Other
- (B) LOCATION: 2...2
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

Cys Xaa Arg Leu Asn Gly Gly Val Ser Met Tyr Val Glu Ser Val Asp  
1 5 10 15  
Arg Tyr Val Cys Arg  
20

15

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

20

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=biotin-Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

25 Xaa Ser Ala Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val  
1 5 10 15  
Arg Leu Asn Gly Val Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser  
20 25 30  
Asn Pro Arg Gly Arg Arg His Pro  
35 40

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

30

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=biotin-Lys(dns)

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

Xaa	Ser	Ser	Ala	Asp	Ala	Glu	Lys	Cys	Ala	Gly	Ser	Leu	Leu	Trp	Trp
1				5					10					15	
Gly	Arg	Gln	Asn	Asn	Ser	Gly	Cys	Gly	Ser	Pro	Thr	Lys	Lys	His	Leu
		20					25						30		
Lys	His	Arg	Asn	Arg	Ser	Gln	Thr	Ser	Ser	Ser	Ser	His			
		35				40						45			

10

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

15

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=biotin-Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

Xaa	Arg	Glu	Phe	Ala	Glu	Arg	Arg	Leu	Trp	Gly	Cys	Asp	Asp	Leu	Ser
1				5					10					15	
Trp	Arg	Leu	Asp	Ala	Glu	Gly	Cys	Gly	Pro	Thr	Pro	Ser	Asn	Arg	Ala
		20					25						30		
Val	Lys	His	Arg	Lys	Pro	Arg	Pro	Arg	Ser	Pro	Ala	Leu			
		35				40						45			

20

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

25

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=biotin-Ser

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

Xaa Gly Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe  
 1 5 10 15  
 Arg Glu Leu Arg Asp Arg Trp Tyr Ala Thr Ser His His Thr Arg Pro  
 20 25 30  
 Thr Pro Gln Leu Pro Arg Gly Pro Asn  
 35 40

(2) INFORMATION FOR SEQ ID NO:274:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

10

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Xaa Ser Gly Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val  
 1 5 10 15  
 Phe Arg Glu Leu Arg Asp Arg Trp Tyr Ala Thr Ser His His Thr Arg  
 20 25 30  
 Pro Thr Pro Gln Leu Pro Arg Gly Pro Asn  
 35 40

(2) INFORMATION FOR SEQ ID NO:275:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=biotin-Lys(dns)

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

Xaa Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe Arg  
 1 5 10 15  
 Glu Leu Arg Asp Arg Trp Asn Ala Thr Ser His His Thr Arg Pro Thr  
 20 25 30  
 Pro Gln Leu Leu Pro Arg Gly Pro Asn  
 35 40

(2) INFORMATION FOR SEQ ID NO:276:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids



(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

5 (A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

Xaa Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe Arg  
1 5 10 15  
Glu Leu Arg Asp Arg Trp Asn Ala Thr Ser His His Thr Arg Pro Thr  
20 25 30  
10 Pro Gln Leu Pro Arg Gly Pro Asn Ser  
35 40

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 45 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

15 (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

20 Xaa Ser Gln Gly Ser Lys Gln Cys Met Gln Tyr Arg Thr Gly Arg Leu  
1 5 10 15  
Thr Val Gly Ser Glu Tyr Gly Cys Gly Met Asn Pro Ala Arg His Ala  
20 25 30  
Thr Pro Ala Tyr Pro Ala Arg Leu Leu Pro Arg Tyr Arg  
35 40 45

(2) INFORMATION FOR SEQ ID NO:278:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 45 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

30 (A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

Xaa Arg Val Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala  
1 5 10 15  
Arg Ser Cys Ala His Gln Gly Cys Gly Ala Gly Thr Arg Asn Ser His  
20 25 30  
Gly Cys Ile Thr Arg Pro Leu Arg Gln Ala Ser Ala His  
35 40 45

5

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=biotin-Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

15 Xaa Ser Gly Ser Gly Arg Val Gly Gln Cys Thr Asp Ser Asp Val Arg  
1 5 10 15  
Arg Pro Trp Ala Arg Ser Cys Ala  
20

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

20

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

Xaa Arg Val Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala  
1 5 10 15  
Arg Ser Cys Ala  
20

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

30

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

Xaa Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val  
1 5 10 15  
Asp Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg  
20 25 30  
Leu Arg Thr Arg Ser Arg Pro Asn Gly  
35 40

10

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

15

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

20 Xaa Arg Gly Ser Thr Gly Thr Ala Gly Gly Glu Arg Ser Gly Val Leu  
1 5 10 15  
Asn Leu His Thr Arg Asp Asn Ala Ser Gly Ser Gly Phe Lys Pro Trp  
20 25 30  
Tyr Pro Ser Asn Arg Gly His Lys  
35 40

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

25

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

Xaa Ser Gly Ser Gly Leu Tyr Ala Asn Pro Gly Met Tyr Ser Arg Leu  
 1 5 10 15  
 His Ser Pro Ala  
 20

(2) INFORMATION FOR SEQ ID NO:284:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- 10 (D) OTHER INFORMATION: Xaa=biotin-Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Xaa Ser Gly Ser Gly Leu Tyr Ala Asn Pro Gly Met Tyr Ser Arg Leu  
 1 5 10 15  
 His Ser Pro Ala  
 20

15 (2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- 20 (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

25 Xaa Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys  
 1 5 10 15  
 Glu Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg  
 20 25 30  
 Lys Val Phe Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr  
 35 40 45

(2) INFORMATION FOR SEQ ID NO:286:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

Xaa	Ser	Pro	Cys	Gly	Gly	Ser	Trp	Gly	Arg	Phe	Met	Gln	Gly	Gly	Leu
1				5				10					15		
Phe	Gly	Gly	Arg	Thr	Asp	Gly	Cys	Gly	Ala	His	Arg	Asn	Arg	Thr	Ser
			20				25					30			
Ala	Ser	Leu	Glu	Pro	Pro	Ser	Ser	Asp	Tyr						
		35				40									

(2) INFORMATION FOR SEQ ID NO:287:

10

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 45 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

15

(A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

Xaa	Arg	Tyr	Lys	His	Asp	Ile	Gly	Cys	Asp	Ala	Gly	Val	Asp	Lys	Lys
1				5				10				15			
Ser	Ser	Ser	Val	Arg	Gly	Gly	Cys	Gly	Ala	His	Ser	Ser	Pro	Pro	Arg
			20				25					30			
20	Ala	Gly	Arg	Gly	Pro	Arg	Gly	Thr	Met	Val	Ser	Arg	Leu		
		35				40						45			

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

25

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

Xaa Ser Ala Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val

1 5 10 15  
 Arg Leu Asn Gly Val Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser  
 20 25 30  
 Asn Pro Arg Gly Arg Arg His Pro Gly Gly  
 35 40

(2) INFORMATION FOR SEQ ID NO:289:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 40 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown  
 (ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:  
 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

Xaa Ser Lys Ser Gly Glu Gly Gly Asp Ser Ser Arg Gly Glu Thr Gly  
 1 5 10 15  
 Trp Ala Arg Val Arg Ser His Ala Met Thr Ala Gly Arg Phe Arg Trp  
 20 25 30  
 Tyr Asn Gln Leu Pro Ser Asp Arg  
 35 40

(2) INFORMATION FOR SEQ ID NO:290:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 41 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown  
 (ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:  
 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

25 Xaa Ser Glu Ala Asn Leu Asp Gly Arg Lys Ser Arg Tyr Ser Ser Pro  
 1 5 10 15  
 Arg Arg Asn Ser Ser Thr Arg Pro Arg Thr Ser Pro Asn Ser Val His  
 20 25 30  
 Ala Arg Tyr Pro Ser Thr Asp His Asp  
 35 40

(2) INFORMATION FOR SEQ ID NO:291:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 44 amino acids  
 (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: Modified Base  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=biotin-S

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

Xaa	Gly	Ser	Gly	Ser	Thr	Pro	Pro	Ser	Arg	Glu	Ala	Tyr	Ser	Arg	Pro
1				5					10					15	
Tyr	Ser	Val	Asp	Ser	Asp	Ser	Asp	Thr	Asn	Ala	Lys	His	Ser	Ser	His
			20					25					30		
Asn	Arg	Arg	Leu	Arg	Thr	Arg	Ser	Arg	Pro	Asn	Gly				
			35					40							

10

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

Xaa	Arg	Val	Gly	Gln	Cys	Thr	Asp	Ser	Asp	Val	Arg	Arg	Pro	Trp	Ala
1				5					10					15	
Arg	Ser	Cys	Ala	His	Gln	Gly									
				20											

20

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

30

Xaa Cys Gly Ala Gly Thr Arg Asn Ser His Gly Cys Ile Thr Arg Pro  
 1 5 10 15  
 Leu Arg Gln Ala Ser Ala His Gly  
 20

(2) INFORMATION FOR SEQ ID NO:294:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown  
 (ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:  
 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 10 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

Xaa Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly  
 1 5 10 15  
 Arg Arg His Pro Gly  
 20

15 (2) INFORMATION FOR SEQ ID NO:295:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 12 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown  
 (ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:  
 20 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

Xaa Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly  
 1 5 10

25 (2) INFORMATION FOR SEQ ID NO:296:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 16 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown  
 (ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:  
 30 (A) NAME/KEY: Other



(  
(  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

Xaa Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly  
1 5 10 15

5

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10

(ix) FEATURE:

(A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

15 Xaa Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg Arg His Pro  
1 5 10 15  
Gly

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg  
1 5 10 15  
Ser Arg Pro Asn  
20

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

15

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

Xaa Ser Ser His Asn Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

25

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

Xaa Ser Ser His Asn Arg Arg Leu Arg Thr Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:302:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

5 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

Xaa Val Arg Arg Pro Trp Ala Arg Ser Cys Ala His Gln Gly Cys Gly  
 1 5 10 15  
 Ala Gly Thr Arg Asn Ser  
 20

10 (2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None  
 (ix) FEATURE:

15 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

Xaa Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala Arg Ser Cys  
 1 5 10 15

20 (2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 41 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

25 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

30 Xaa Ser Arg Ala Asn Thr Asp Gly Arg Lys Ser Arg Tyr Ser Ser Pro  
 1 5 10 15  
 Arg Arg Asn Ser Ser Thr Glu Pro Arg Leu Ser Pro Asn Ser Val His

Ala Arg Tyr Pro Ser Thr Asp His Asp  
 20 25  
 35 40

30

(2) INFORMATION FOR SEQ ID NO:305:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:  
 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

Xaa Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:306:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:  
 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

Xaa Ser Asn Pro Arg Gly Arg Arg His Pro Gly  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:307:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:  
 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

Xaa Glu Asn Ala Asn Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:308:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- 10 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

Xaa Ala Asn Thr Arg Lys Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:309:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- 20 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

Xaa Thr Arg Lys Ser Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:310:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- 30 (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

Xaa Arg Lys Ser Ser Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:311:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

10

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

Xaa Lys Ser Ser Arg Ser Asn  
1 5

(2) INFORMATION FOR SEQ ID NO:312:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

20

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

Xaa Ser Ser Arg Ser Asn Pro Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:313:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

30

- (A) NAME/KEY: Other

(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

Xaa Arg Ser Asn Pro Arg Gly  
1 5

5

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

Xaa Ser Asn Pro Arg Gly  
1 5

15

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

Xaa Pro Arg Gly Arg Arg His  
1 5

25

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

30

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

5 Xaa Arg Arg His Pro Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

10 (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

15 Xaa Lys Ser Ser Arg Gly Asn  
1 5

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

25 Xaa Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro Gly  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

30 (ii) MOLECULE TYPE: peptide



(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

5

Xaa Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg Arg His Pro  
1 5 10 15  
Gly

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

Xaa Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg Arg His Pro  
1 5 10 15  
Gly

(2) INFORMATION FOR SEQ ID NO:321:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

25

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

Xaa Thr Asn Ala Lys His Ser Ser His Asn  
1 5 10

30

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

5 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

Xaa Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn  
 1 5 10

10 (2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 9 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

15 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

Xaa Arg Arg Leu Arg Thr Arg Ser Arg  
 1 5

20 (2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 7 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

25 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

Xaa Arg Arg Leu Arg Thr Arg  
 1 5

30 (2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

5 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

Xaa Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn  
 1 5 10

10 (2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 27 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

15 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

Xaa Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys  
 1 5 10 15  
 20 Glu Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly  
 20 25

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 28 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

25 (ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

(A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

30 Xaa Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg Lys

1 5 10 15  
 Val Phe Asn Arg Arg Pro Ser Ala Ile Pro Thr  
 20 25

(2) INFORMATION FOR SEQ ID NO:328:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:  
 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

Xaa Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys  
 1 5 10 15  
 Glu Pro Gly Cys  
 20

(2) INFORMATION FOR SEQ ID NO:329:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 14 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

- 20 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

Xaa Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:330:

25

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

30

- (A) NAME/KEY: Other  
 (B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

Xaa Arg Lys Val Phe Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr  
1 5 10 15

5 (2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

10

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

Xaa Arg Lys Val Phe Asn Arg Arg Arg Pro Ser  
1 5 10

15

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

20

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

Xaa Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr  
1 5 10

25

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

30

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

5 Xaa Asn Arg Arg Arg Pro Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

10 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp  
1 5 10 15  
Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu  
20 25 30  
Arg Thr Arg Ser Arg Pro Asn Gly  
35 40

15 (2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys Glu  
1 5 10 15  
Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg Lys  
20 25 30  
Val Phe Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr  
35 40

25 (2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

30 (A) NAME/KEY: Other  
(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

5 Xaa Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys  
1 5 10 15  
Glu Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr  
20 25 30

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

10 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

15 Xaa Asn Leu Arg Ser Asp Asn Ala Lys Glu Pro Gly Asp Tyr Asn Cys  
1 5 10 15  
Cys Gly Asn Gly Asn Ser Thr Gly Arg Lys Val Phe Asn Arg  
20 25 30

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

20 (C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg  
1 5 10 15  
Lys Val Phe Asn Arg Arg Pro Ser Ala Ile Pro Thr  
20 25

(2) INFORMATION FOR SEQ ID NO:339:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

Xaa Ala Ser His Asn Arg Arg Leu Arg Thr Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:340:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

Xaa Ser Ala His Asn Arg Arg Leu Arg Thr Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:341:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

Xaa Ser Ser Ala Asn Arg Arg Leu Arg Thr Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:342:

30 (i) SEQUENCE CHARACTERISTICS:



(

(A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

5 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

Xaa Ser Ser His Ala Arg Arg Leu Arg Thr Arg  
 1 5 10

10 (2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

15 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

Xaa Ser Ser His Asn Ala Arg Leu Arg Thr Arg  
 1 5 10

20 (2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

25 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

Xaa Ser Ser His Asn Arg Ala Leu Arg Thr Arg  
 1 5 10

30 (2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

5 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

Xaa Ser Ser His Asn Arg Arg Ala Arg Thr Arg  
 1 5 10

10 (2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

15 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Xaa Ser Ser His Asn Arg Arg Leu Ala Thr Arg  
 1 5 10

20 (2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

25 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

30 Xaa Ser Ser His Asn Arg Arg Leu Arg Ala Arg  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

10 Xaa Ser Ser His Asn Arg Arg Leu Arg Thr Ala  
1 5 10

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

15 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

Ser Ser His Asn Arg Arg Leu Arg Thr Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

Xaa Gly Arg Asn His Asp Val Val Ser Ser Asn Thr His Lys Ser Tyr  
1 5 10 15  
Arg Ser Pro Arg Ser Ala Ser Tyr Pro Arg Leu Ser Asn Asp Arg Thr  
20 25 30  
30 Asp Arg Thr Glu Pro Ala Pro Ser Ser  
35 40

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

10 Xaa Arg Asn Thr Arg Asn Lys Thr Ser Arg Leu Ser Ala Asn Pro His  
1 5 10 15  
Arg Ser His Arg  
20

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

15

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 20...20
- (D) OTHER INFORMATION: Xaa=Lys(dns)

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg Ser  
1 5 10 15  
Arg Pro Asn Xaa  
20

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

25

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 10...10
- (D) OTHER INFORMATION: Xaa=Lys(dns)

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

Arg Arg Leu Arg Thr Arg Ser Arg Lys Xaa  
1 5 10

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

Xaa Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys  
1 5 10 15  
Glu Pro Gly Asp Tyr  
20

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

Xaa Ser Asp Asn Ala Lys Glu Pro Gly Asp Tyr Asn Cys Cys Gly Asn  
1 5 10 15  
Gly Asn Ser Thr Gly  
20

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

**5** Xaa Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

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10      (ii) MOLECULE TYPE: peptide
      (ix) FEATURE:

```

(A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

15 Xaa Glu Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

25 Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

30 (D) TOPOLOGY: unknown  
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

5

Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: MEMORY
- (B) STRAIN: DISPLAY MEMORY

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

Xaa Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

20

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

Xaa Lys Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg Arg His  
1 5 10 15  
Pro Gly

30

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 18 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

5 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

Xaa Lys Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg Arg His  
 1 5 10 15  
 10 Pro Gly

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

15 (ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

(A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

20 Xaa Lys Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr  
 1 5 10 15  
 Arg

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 16 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

25 (ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

(A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:



Xaa Thr Asn Ala Lys His Ser Ser Cys Asn Arg Arg Cys Arg Thr Arg  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

Xaa Thr Asn Ala Lys His Ser Ser Cys Asn Arg Arg Leu Arg Cys Arg  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

Xaa Ala Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

Xaa Thr Ala Ala Lys Asn Ser Ser His Asn Arg Arg Leu Arg Thr Arg  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:368:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

10 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

Xaa Thr Asn Gly Lys Asn Ser Ser His Asn Arg Arg Leu Arg Thr Arg  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:369:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

20 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

Xaa Thr Asn Ala Lys Ala Ser Ser His Asn Arg Arg Leu Arg Thr Arg  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:370:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

30 (B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

Xaa Thr Asn Ala Lys His Ala Ser His Asn Arg Arg Leu Arg Thr Arg  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:371:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

10

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

Xaa Thr Asn Ala Lys His Ser Ala His Asn Arg Arg Leu Arg Thr Arg  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:372:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

20

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

Xaa Thr Asn Ala Lys His Ser Ser Ala Asn Arg Arg Leu Arg Thr Arg  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:373:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

30

(A) NAME/KEY: Other

(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

Xaa Thr Asn Ala Lys His Ser Ser His Ala Arg Arg Leu Arg Thr Arg  
1 5 10 15

5

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10

(ix) FEATURE:

(A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

15 Xaa Thr Asn Ala Lys His Ser Ser His Asn Ala Arg Leu Arg Thr Arg  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20

(ix) FEATURE:

(A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

25 Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Ala Leu Arg Thr Arg  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

30

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(  
(  
(A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

5 Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Ala Arg Thr Arg  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

10 (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

15 Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Ala Thr Arg  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

25 Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Ala Arg  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

30 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

5

Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Ala  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

15

Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

20

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

25

Xaa Lys Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr  
1 5 10 15  
Arg

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid

30

(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:383:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

Xaa Lys Ser Ser His Asn Arg Arg Leu Arg Thr Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:384:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

Xaa Lys Ser Ser His Asn Arg Arg Leu Arg Thr Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:385:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

5 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

Xaa Lys Thr Asn Ala Lys His Ser Ser His Asn Arg  
 1 5 10

10 (2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 12 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

15 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

Xaa Lys Thr Asn Ala Lys His Ser Ser His Asn Arg  
 1 5 10

20 (2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 16 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

25 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg  
 1 5 10 15

30 (2) INFORMATION FOR SEQ ID NO:388:



(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

5 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

Xaa Ala Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly  
 1 5 10 15

10 (2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

15 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

Xaa Pro Ala Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly  
 1 5 10 15

20 (2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

25 (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

30 Xaa Pro Gly Ala Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

- 5 (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

10 Xaa Pro Gly Asp Ala Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

- 15 (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

20 Xaa Pro Gly Asp Tyr Ala Cys Cys Gly Asn Gly Asn Ser Thr Gly  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

- 25 (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

30 Xaa Pro Gly Asp Tyr Asn Ala Cys Gly Asn Gly Asn Ser Thr Gly

1

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10

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## (2) INFORMATION FOR SEQ ID NO:394:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

5

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

Xaa Pro Gly Asp Tyr Asn Cys Ala Gly Asn Gly Asn Ser Thr Gly  
1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:395:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

15

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

Xaa Pro Gly Asp Tyr Asn Cys Cys Ala Asn Gly Asn Ser Thr Gly  
1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:396:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

25

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Ala Gly Asn Ser Thr Gly  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Ala Asn Ser Thr Gly  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Ala Ser Thr Gly  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ala Thr Gly  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

- 10 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Ala Gly  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

- 20 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Ala  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

30 Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

Pro Gly Asp Tyr Asn Cys Cys Gly Asn Cys Asn Ser Thr Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 40 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

15 Ser Ala Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val Arg  
1 5 10 15  
Leu Asn Gly Val Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn  
20 25 30  
Pro Arg Gly Arg Arg His Pro Gly  
35 40

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 19 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

25 Gly Thr Arg Asn Ser His Gly Cys Ile Thr Arg Pro Leu Arg Gln Ala  
1 5 10 15  
Ser Ala His

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

30 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

5 Xaa Arg Val Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala  
1 5 10 15  
Arg Ser Cys Ala His  
20

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 23 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Xaa=Lys(dns)

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

Xaa Cys Gly Ala Gly Thr Arg Asn Ser His Gly Cys Ile Thr Arg Pro  
1 5 10 15  
Leu Arg Gln Ala Ser Ala His  
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